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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 22:16:05 ; Search time 1037 Seconds
(without alignments)
703.635 Million cell updates/sec

Title: US-10-070-882A-2
Perfect score: 139
Sequence: 1 ggcactcgtgcagcaact.....ctgtcttattgttaacaca 139

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	139	4	Aaf82356 Salmonell
2	139	100.0	2802	12	ADG31136 Salmonell
3	40	28.8	41	6	ABL57265 Escherich
4	37.2	26.8	1385	8	ACA49482 Prokaryot
5	32.6	23.5	266145	10	ADB87477 Fowlipox v
6	31	22.3	772	6	ABQ72598 Human MDD
7	31	22.3	810	6	ABQ72685 Human MDD
8	30.8	22.2	19521	8	AaK81193 Human imm
9	30.8	22.2	19521	8	ADA41637 Human sec
10	30.8	22.2	19521	10	ADA57769 BAC fragm
11	30.6	22.0	1539	8	ACA02032 C. glutam
12	30.6	22.0	2799	5	AaH67957 C glutami
13	30.6	22.0	349980	5	AaH85533 C glutami
14	30.4	21.9	31241	10	AAU63315 Mycoplasma
15	30.4	21.9	31241	10	ACC69145 M. genital
16	30.4	21.9	31241	12	ADN48950 Mycoplasma
17	30.4	21.9	104644	6	ABQ99653 Human MS4
18	30.2	21.7	110000	9	ADB12064 03 Continuation (4 of
19	30	21.6	622	12	ADJ38283 Plastid d
20	30	21.6	10711	4	AAK74790 Human imm
21	29.8	21.4	301	3	AAA06526 Human imm

c 95 28.2 20.3 2307 2 AAV43009 Streptococ
c 96 28.2 20.3 2787 2 AAZ96363
c 97 28.2 20.3 3005 4 AAD20313 Streptoco
c 98 28.2 20.3 3563 10 ADE58284 Human gen
c 99 28.2 20.3 3798 2 AAQ2424 Adq42424 AD42 DNA.
c 100 28.2 20.3 5311 10 ADD29639 Add29639 Mouse tum

ALIGNMENTS

RESULT 1
AAAF82356
ID AAF82356 standard; DNA; 139 BP.
XX
AC AAF82356;
XX
DT 22-JUN-2001 (first entry)
XX DE
XX Salmonella typhimurium phoP gene promoter.
XX DE
XX Salmonella typhimurium; phoP gene promoter; PphoP; antibacterial;
KW antiviral; vaccine; lacZ; pggC; outer membrane porin C; ompC;
KW transgenic microorganism; antigen production; antigen delivery;
KW infection; ds.
XX
XX Salmonella typhimurium.
XX OS
XX WO200119974-A2.
XX PN
XX 22-MAR-2001.
XX PD
XX 06-SEP-2000; 2000WO-GB003402.
XX PF
XX 10-SEP-1999; 99GB-00021275.
XX PR
XX 12-JUL-2000; 2000GB-00017000.
XX PR
XX (MINA) UK SEC FOR DEFENCE.
XX PA
XX Titball RW, Bullifent HJ;
XX PI
XX WPI; 2001-328017/34.
XX DR
XX
XX New recombinant gut-colonizing microorganism, useful as vaccine
PT component, comprises construct containing phoP, pagC or ompC gene
PT promoter linked to nucleic acid encoding protein that induces immune
PT response against pathogen.
XX
XX Claim 1; Fig 6; 33pp; English.
XX PS
XX The present sequence is a DNA fragment comprising the phoP gene promoter.
CC DNA fragments comprising the Salmonella typhimurium phoP, pagC and ompC
CC gene promoters were integrated into a vector used to transform a
CC recombinant gut-colonising microorganism. The promoter was operably
CC linked to a nucleic acid encoding a protein that is able to induce a
CC protective immune response against an organism in a mammal. The construct
CC is useful for enhancing expression of a desired protein at mucosal
CC effector sites. It is useful for delivering a variety of antigenic agents
CC which can be used to induce a protective immune response against a wide
CC range of pathogens such as bacillus anthracis, Bordetella pertussis,
CC Schistosoma mansoni, herpes simplex virus, and Mycobacterium tuberculosis.
CC The three promoters (P(phoP), P(pagC) and P(ompC)) are induced at
CC different stages in the infection process, and hence at different sites
CC in the body. This approach allows the induction of different immune
CC responses which provide protection against pathogens which colonise
CC different host cell compartments. The Salmonella vaccine vector system is
CC ideally suited to the delivery of many vaccine antigens since the vaccine
CC delivery mechanism accurately mimics the natural disease, entering the
CC body via the gut
XX
XX Sequence 139 BP; 37 A; 33 C; 23 G; 46 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 139; DB 4; Length 139;

Best Local Similarity 100.0%; Pred. No. 5.6e-36;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACTCTGTCGACGAACCTTAATAATGCGCTGCCTCACCTCTTTCTTCAGAAAGAGG 60
DB 1 GTGACTCTGTCGACGAACCTTAATAATGCGCTGCCTCACCTCTTTCTTCAGAAAGAGG 60
QY 61 GTGACTATTGCTGCTTTTATTAACTGTTTATCCCAAGACCACTAATCAACGCTAGAC 120
DB 61 GTGACTATTGCTGCTTTTATTAACTGTTTATCCCAAGACCACTAATCAACGCTAGAC 120
QY 121 TGTTCCTATTGTTAAACACA 139
DB 121 TGTTCCTATTGTTAAACACA 139

RESULT 2

ADG31136
ID ADG31136 standard; DNA; 2802 BP.
XX
AC ADG31136;
XX
DT 26-FEB-2004 (first entry)
XX DE
XX Salmonella typhimurium PphoPQ and phoPQ operon DNA.
XX DE
XX live attenuated derivative; pathogenic Enterobacteriaceae;
KW cross protective immunity; antibacterial; immunostimulant; vaccine;
KW PphoPQ; promoter; phoPQ operon; ds; gene.
XX
XX Salmonella typhimurium.
XX OS
XX WO2003096812-A1.
XX PN
XX 27-NOV-2003.
XX PD
XX 15-APR-2003; 2003WO-US011802.
XX PF
XX 15-APR-2002; 2002US-0372616P.
XX PR
XX 18-APR-2002; 2002US-0373626P.
XX PR
XX (UNIW) UNIV WASHINGTON.
XX PA
XX Curtiss R;
XX PI
XX WPI: 2004-042484/04.
XX DR
XX P-PSDB; ADG31137, ADG31138, ADG31139.

XX New live attenuated derivative of a pathogenic Enterobacteriaceae
PT species, useful as a vaccine for inducing cross protective immunity
PT against infections caused by various Enterobacteriaceae strains or
PT serotypes.

XX Example 17; Fig 28; 133pp; English.

XX The invention relates to a novel live attenuated derivative of a
CC pathogenic Enterobacteriaceae species having enhanced ability to induce
CC cross protective immunity against Enterobacteriaceae. The derivative of
CC the invention demonstrates antibacterial and immunostimulant activities
CC and may be useful as a vaccine for inducing a high level immune response
CC and/or cross protective immune response to protect individuals from
CC infection from a diversity of species or serotypes of bacterial
CC pathogens. The current sequence is that of the Salmonella typhimurium
CC PphoPQ and phoPQ operon DNA of the invention.

XX Sequence 2802 BP; 721 A; 702 C; 724 G; 655 T; 0 U; 0 Other;

Query Match 100.0%; Score 139; DB 12; Length 2802;

Best Local Similarity 100.0%; Pred. No. 1.3e-35;

Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACTCTGTCGACGAACCTTAATAATGCGCTGCCTCACCTCTTTCTTCAGAAAGAGG 60

Db 511 GTGACTCTGGTCGACGAACCTTAATAATGCGTCGCTCACCCCTCTTTCTTCAGAAAGAGG 570
QY 61 GTGACTATTGCTGCTGTTTATTAACTGTTTATCCCCCAAGACCAATCAACGCTAGAC 120
|||||
Db 571 GTGACTATTGCTGCTGTTTATTAACTGTTTATCCCCCAAGACCAATCAACGCTAGAC 630
|||||
QY 121 TGTTCCTATTGTTAAACACA 139
|||||
Db 631 TGTTCCTATTGTTAAACACA 649
|||||
RESULT 3
ABL57265
ID ABL57265 standard; DNA; 41 BP.
XX AC
XX ABL57265;
XX
DT 09-AUG-2002 (first entry)
XX
DE Escherichia coli DNA 5' to phoA coding region.
XX
KW Transcription terminator; trpA; attenuation; vaccine; virucide;
KW antibacterial; fungicide; antiparasitic; protozoacide; phoA; ds.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT misc_feature 1..19
FT /*tag= a
FT /note= "5' single-stranded overhang"
FT misc_feature 41
FT /*tag= b
FT /note= "5' overhang on complementary strand of 4 bases
FT with sequence 5'-GATC-3'"
XX
PN WO200230457-A2.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-US031606.
XX
PR 12-OCT-2000; 2000US-00689123.
XX
XX (UNIW) UNIV WASHINGTON.
PA (MEGA-) MEGAN HEALTH INC.
PA (CURT/) CURTISS R.
PA (TING/) TINGE S A.
XX
PI Curtiss R, Tinge SA;
XX
DR WPI; 2002-444150/47.
XX
XX Composition comprising microbe having attenuating mutation that comprises
PT insertion sequence containing recombinant transcription terminator,
PT useful as vaccine, and for delivering a desired gene product to
PT individual.
XX
XX Example 5; Fig 11; 91pp; English.
XX
CC The present sequence is that of DNA located 5' to the phoA coding
CC sequence of Escherichia coli. The sequence was used to illustrate an
CC example of the invention relating to deletion of the phoA gene and
CC replacement with a trpA terminator. The phoA mutation was introduced into
CC Salmonella typhimurium SL1344 to produce strain MGN-1362. The present
CC invention is based on the discovery that transcription terminators (TTs)
CC can be inserted in a bacterial gene in an attenuating strategy which not
CC only attenuates the virulence of the bacteria, but also serves to
CC restrict the effect of the attenuating mutation to the target gene or
CC operon of the bacteria. A claimed vaccine comprises a microorganism
CC having an attenuating mutation in a chromosomal gene, the mutation
CC comprising an insertion sequence which contains a recombinant TT, such as
CC trpA. The microorganism is preferably Salmonella, Shigella or
CC Escherichia, and the TT is preferably inserted in the phoP gene. The

CC vaccine may further comprise a recombinant gene encoding a desired gene
CC product from a virus, bacterium, protozoan, parasite or fungus, or
CC encodes an autoantigen, gamete-specific antigen or an allergen. The
CC attenuated microorganism is also used in a claimed method for delivering
CC a desired gene product to an individual
XX
SQ Sequence 41 BP; 10 A; 13 C; 4 G; 14 T; 0 U; 0 Other;
Query Match 28.8%; Score 40; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCGACGAACCTTAATAATGCGTCGCTCACCCCTCTTTCTT 50
|||||
Db 1 TCGACGAACCTTAATAATGCGTCGCTCACCCCTCTTTCTT 40
|||||
RESULT 4
ACA49482
ID ACA49482 standard; DNA; 1385 BP.
XX
XX ACA49482;
XX AC
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #31139.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
XX OS Salmonella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-0007285A.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU45612.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 37352; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1385 BP; 353 A; 372 C; 335 G; 321 T; 0 U; 4 Other;

Query Match 26.8%; Score 37.2; DB 8; Length 1385;
 Best Local Similarity 92.9%; Pred. No. 0.048; Mismatches 0; Gaps 0;
 Matches 39; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GTGACTCTGTGCGAGCACTTAATAATGCTGCTCACCCCT 42
 |||||
 Db 1344 GTGACTCTGTGCGAGCACTTAATAATGCTGCTCACCCCT 1385

RESULT 5

ADBE87477
 ID ADE87477 standard; DNA; 266145 BP.

XX ADE87477;

DT 29-JAN-2004 (first entry)

XX Fowlpox virus genome DNA.

KW fowlpox virus; FPV; virucide; tuberculostatic; protozoacide; antipyrretic;
 KW cytosatic; hepatotropic; antibacterial; vaccine; malaria; tuberculosis;
 KW East Coast fever; avipox virus; influenza; hepatitis;
 KW human papilloma virus; tumour; leishmaniasis; listeriosis; theileria;
 KW gene; ds.

XX Fowlpox virus.

OS WO2003047617-A2.

PN 12-JUN-2003.

PD 02-DEC-2002; 2002WO-GB005411.

PF 30-NOV-2001; 2001GB-00028733.

XX 30-NOV-2001; 2001US-0334649P.

XX (ISIS-) ISIS INNOVATION LTD.

XX Laidlaw S, Skinner M, Hill A, Gilbert S, Anderson R;

XX WPI; 2003-513700/48.

XX Treating and/or preventing e.g. malaria or tuberculosis, or eliciting an
 PT immune response, comprises administering a priming composition and a
 PT boosting composition containing a non-replicating viral vector in either
 PT order.

XX Claim 30; SEQ ID NO 1; 302pp; English.

XX The invention relates to a fowlpox virus (FPV) genome which has
 CC modifications in one or more wild-type FPV genes. The invention further
 CC relates to a novel method for treating and/or preventing a disease in a
 CC subject comprising administering two compositions, each containing a non-
 CC replicating viral vector. At least one of the compositions comprises a

CC poxvirus vector derived from a fowlpox virus. The novel compositions have
 CC the following activities: virucide, tuberculostatic, protozoacide,
 CC antipyrretic, cytosatic, hepatotropic, and antibacterial. The non-
 CC replicating viral vector is useful in a vaccine for an animal,
 CC particularly a mammal such as a primate, specifically human. The priming
 CC or boosting composition, or the kit is useful for manufacturing a
 CC medicament for treating and/or preventing a disease which is, or results
 CC from, a chronic infection such as malaria, tuberculosis or East Coast
 CC fever, or for eliciting a T-cell immune response in a subject. Non-
 CC cultured CEP cells are useful for growing an avipox virus, such as
 CC fowlpox virus. The method or the vaccine may further be used to treat or
 CC prevent influenza, hepatitis, human papilloma virus and other viral
 CC infections, malignancies such as tumours, leishmaniasis, listeriosis, and
 CC theileria. This polynucleotide sequence represents the DNA of the fowlpox
 CC virus genome of the invention.

SQ Sequence 266145 BP; 92375 A; 41026 C; 40846 G; 91897 T; 0 U; 1 Other;

Query Match 23.5%; Score 32.6; DB 10; Length 266145;

Best Local Similarity 55.9%; Pred. No. 7;
 Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 18 ACTTAATAATGCTGCTCACCCCTCTTTCTTCAGAAAGAGGTGACTATTGTCTGGT 77

Db 21181 AGTTACTTATAGATATATTTTAATATCTTATCGACGGAAGGACGATCCATGTTATG 21240

QY 78 TTATTAACCTGTTTATCCCAAGACCAATAATCAACGCTAGACTGTTCTTTA 128

Db 21241 TTATGATGTTTCTGCTCAATAAAGGGTAATGATCAATACTATAATGTTTATA 21291

RESULT 6

ABQ72598/C

ID ABQ72598 standard; cDNA; 772 BP.

XX ABQ72598;

XX 03-SEP-2002 (first entry)

DE Human MDDT encoding cDNA SEQ ID NO 150.

XX Human; MDDT; disease detection and treatment molecule polynucleotide;
 KW proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
 KW autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
 KW rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; antipeptidic; cytosatic; anti-HIV;
 KW antiallergic; antianemic; antiasthmatic; antiatherosclerotic; antigout;
 KW neuroprotective; antirheumatic; antiarthritic; gene; ss.

OS Homo sapiens.

PN WO200240715-A2.

XX 23-MAY-2002.

PD 06-SEP-2001; 2001WO-US027628.

XX 05-SEP-2000; 2000US-0229747P.

PR 05-SEP-2000; 2000US-0229748P.

PR 05-SEP-2000; 2000US-0229749P.

PR 05-SEP-2000; 2000US-0229750P.

PR 05-SEP-2000; 2000US-0229751P.

PR 06-SEP-2000; 2000US-0230583P.

PR 06-SEP-2000; 2000US-0230514P.

PR 06-SEP-2000; 2000US-0230515P.

PR 06-SEP-2000; 2000US-0230517P.

PR 06-SEP-2000; 2000US-0230519P.

PR 06-SEP-2000; 2000US-0230595P.

PR 06-SEP-2000; 2000US-0230597P.

PR 06-SEP-2000; 2000US-0230598P.

PR 06-SEP-2000; 2000US-0230599P.

CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I), and for
 CC preparing a polyclonal or monoclonal antibody by hybridoma technology.
 CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
 CC screening a compound for effectiveness in altering expression of a target
 CC polynucleotide comprising. Oligonucleotides and antibodies are useful for
 CC detecting MDP in a sample or for assessing toxicity of a test compound,
 CC in a diagnostic test for a condition or a disease associated with the
 CC expression of MDP in a biological sample, for detecting (I) in a sample,
 CC and for purifying (I) from a sample. A composition comprising (I), an
 CC agonist or antagonist is useful for treating a disease or condition
 CC associated with decreased or increased expression of functional MDP. (I)
 CC or (II) are useful for diagnosing, treating or preventing disorders
 CC associated with aberrant expression of MDP, where the disorders are
 CC selected from a cell proliferative disorder such as arteriosclerosis,
 CC cirrhosis, hepatitis, psoriasis, and cancer and an
 CC autoimmune/inflammatory disorder such as AIDS, Addison's disease,
 CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
 CC rheumatoid arthritis. (II) are useful for creating knockin humanised
 CC animals or transgenic animals to model human diseases, in somatic or
 CC germline gene therapy, to generate a transcript image of a tissue or cell
 CC type, for detecting differences in the chromosomal location due to
 CC translocation or inversion among normal, carrier or affected individuals
 CC and as hybridisation probes for mapping naturally occurring genomic
 CC sequences
 CC
 SQ Sequence 810 BP; 262 A; 153 C; 165 G; 230 T; 0 U; 0 Other;

Query Match 22.38; Score 31; DB 6; Length 810;
 Best Local Similarity 57.94; Pred. No. 4.6;
 Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 Qy 45 TTTCTTCAGAAAGGGTGACTATTTCCTGGTTTATTAACCTGTTATCCCAAGCACC 104
 Db |||||
 549 TTCAATATAAAAGGCTCCATTAGTTATTTATCATCAGTTTGTCACAAAGCGCT 490
 Qy 105 ATAATCAACCTAGACTGTTCTTATTTGTTTAAACA 139
 Db |||||
 489 TTCTGTAATGCTAGAAATCTCAGTGTCAACACA 455

RESULT 8
 AAK81193/c
 ID AAK81193 standard; DNA; 19521 BP.
 XX
 AC AAK81193;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36005.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytotatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US0001354.

XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225477P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226688P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 30-AUG-2000; 2000US-0227009P.
 PR 01-SEP-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.

XX 19-DEC-2002.
XX 13-JUN-2001; 2001DE-01028510.
XX 13-JUN-2001; 2001DE-01028510.
XX 13-JUN-2001; 2001DE-01028510.
XX (DEGS) DEGUSSA AG.
XX Farwick M, Moeckel B, Pfeifferle W, Bathe B, Ruthmacher K;
XX WPI; 2003-279970/28.
XX New nucleic acid array useful for monitoring mRNA expression of
PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
PT from Corynebacterium glutamicum.
XX Claim 1; Page 665-666; 709pp; German.
XX This invention describes a novel nucleic acid array involving
CC Corynebacterium glutamicum polynucleotides. The arrays are used to
CC analyse C. glutamicum, particularly for monitoring a fermentation process
CC to determine expression levels of C. glutamicum cellular mRNA. Such
CC monitoring particularly differentiates between expression levels of
CC different strains of C. glutamicum and allows the adjustment of different
CC culture and fermentation conditions. ACA00010-ACA02188 represent C.
CC glutamicum derived polynucleotides described in the disclosure of the
CC invention
XX
SQ Sequence 1539 BP; 393 A; 394 C; 414 G; 338 T; 0 U; 0 Other;
Query Match 22.0%; Score 30.6; DB 8; Length 1539;
Best Local Similarity 53.8%; Pred. No. 7.5;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 17 AACTTAAATAGCGCTGCCTCACCCTCTTTCTTCAGAAAGAGGGTGACTATTGTCTGG 76
DB 241 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAGAACTCAACCCATTGGTGG 300
QY 77 TTTATTAACTGTTTATCCCAAGACCAATAATCAACGGCTAGACTGTTCTATTGTT 133
DB 301 ATCATGCACAGTCTGTTTCACACCAACCAANTTCCCGATCCACGATGATCGGT 357
RESULT 12
AAH67957
ID AAH67957 standard; DNA; 2799 BP.
XX
AC AAH67957;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 2992.
XX
KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
XX Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000EP-00127688.
XX
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
PI

XX WPI; 2001-376931/40.
DR P-PSDB; AAG92738.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 2992; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 2799 BP; 715 A; 731 C; 728 G; 625 T; 0 U; 0 Other;
Query Match 22.0%; Score 30.6; DB 5; Length 2799;
Best Local Similarity 53.8%; Pred. No. 8.9;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 17 AACTTAAATAGCGCTGCCTCACCCTCTTTCTTCAGAAAGAGGGTGACTATTGTCTGG 76
DB 271 AACGTCATTGATGGCAGCGAAGGCATGCTTCATGCAGAGAACTCAACCCATTGGTGG 330
QY 77 TTTATTAACTGTTTATCCCAAGACCAATAATCAACGGCTAGACTGTTCTATTGTT 133
DB 331 ATCATGCACAGTCTGTTTCACACCAACCAANTTCCCGATCCACGATGATCGGT 387
RESULT 13
AAH68533/c
ID AAH68533 standard; DNA; 349980 BP.
XX
AC AAH68533;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7068.
XX
KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
XX Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000EP-00127688.
XX
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
PI
XX WPI; 2001-376931/40.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.

XX Disclosure; SEQ ID NO 7068; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

CC sequences from the Corynebacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of corynebacterium, measuring expression amount and analysing

CC the expression profile or expression pattern of a gene derived from

CC Corynebacterium, and identifying a homologue of a gene derived from

CC Corynebacterium. Corynebacterium bacteria are useful for producing amino

CC acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a nucleic acid described

CC in the exemplification of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from the European Patent Office

XX

XX Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;

Query Match 22.0%; Score 30.6; DB 5; Length 349980;

Best Local Similarity 53.8%; Pred. No. 35;

Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 17 AACTTAATAATGCTGCTCCCTCAACCTCTTTCTTCAGAAAGAGGGTGACTATTGTCTGG 76

Db 200056 AACGTCATTGATGCGACGAGGCGATGCTTCATGCGAGAACTCAACCCATTGGTTGG 199997

Qy 77 TTTATTAACTGTTTATCCCAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133

Db 199996 ATCATCGACAGTGCTGTTTCACACCAACCAATTCACGATCCAACTGATGATCGGT 199940

RESULT 14

AD63515/c

ID AAD63515 standard; DNA; 31241 BP.

XX

XX AAD63515;

XX

DT 12-FEB-2004 (first entry)

XX

DE Mycoplasma genitalium gene involved in transport and binding.

XX

XX Genetic operating system; nanomachine genome; bioreactor; bioremediation;

XX therapeutic biomolecule; energy conversion system; processing system;

XX anabolic; catabolic system; biological film; cosmetic application;

XX coating; ds.

XX

OS Mycoplasma genitalium.

XX

PN US2003138777-A1.

XX

PD 24-JUL-2003.

XX

PF 20-SEP-2001; 2001US-00960858.

XX

PR 20-SEP-2001; 2001US-00960858.

XX

PA (EVAN/) EVANS G A.

XX

PI Evans GA;

XX

DR WPI; 2003-851721/79.

XX

XX Basic genetic operating system for an autonomous prototrophic

PT nanomachine, comprises a nanomachine genome encoding a minimal gene set.

XX

XX Example 1; Page 127-141; 170pp; English.

XX

XX The invention relates to a basic genetic operating system which comprises

CC a nanomachine genome encoding a minimal gene set for viability. The basic

CC genetic operating system is used for an autonomous prototrophic

CC nanomachine or autonomous autotrophic nanomachine. The nanomachine is

CC used as a bioreactor, for bioremediation, for production of a therapeutic

CC biomolecule or as therapeutic agent, for production of a diagnostic

CC indicator or as a diagnostic reagent, as a delivery system, as an

CC artificial tissue or organ system, an energy conversion system, as a

CC processing system, as an anabolic or catabolic system, for production of

CC biological films or coatings that may respond to the environment and for

CC cosmetic applications including pharmaceuticals. The present sequence is

XX Mycoplasma genitalium nanomachine gene

XX

SQ Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;

Query Match 21.9%; Score 30.4; DB 10; Length 31241;

Best Local Similarity 55.8%; Pred. No. 20;

Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 34 CCTCACCTCTTTCTTCAGAAAGAGGGTGACTATTGTCTGTTTATTAACTGTTATC 93

Db 25866 CCTCAGCCAAATTTTTTTAAACCAAGGTGGAGTTTACCATCTGTTTCTTCTTGT 25807

Qy 94 CCCAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAAACA 137

Db 25806 ATTAAAGAACGCTATCAATCTATACCCCTTTTGTGCTAAAA 25763

RESULT 15

ACC69145/c

ID ACC69145 standard; DNA; 31241 BP.

XX

XX ACC69145;

XX

DT 10-JUL-2003 (first entry)

XX

DE M. genitalium transport and binding gene cassette DNA SEQ ID NO:13.

XX

XX Mycoplasma genitalium; gene cassette; replication; transcription;

XX translation; metabolism; basic genetic operating system; gene therapy;

XX autonomous prototrophic nanomachine; autotrophic nanomachine;

XX nanomachine; bioreactor; bioremediation; therapeutic; delivery system;

XX artificial tissue; artificial organ system; energy conversion system;

XX processing system; anabolic system; catabolic system; biological film;

XX biological coating; cosmetic; gene; ds.

XX

OS Mycoplasma genitalium.

XX

PN WO2003025145-A2.

XX

PD 27-MAR-2003.

XX

PF 18-SEP-2002; 2002WO-US029811.

XX

PR 20-SEP-2001; 2001US-00960870.

XX

PA (EGEA-) EGEA BIOSCIENCES INC.

XX

PI Evans GA;

XX

DR WPI; 2003-354602/33.

XX

XX New basic genetic operating system for autonomous prototrophic or

PT autotrophic nanomachine, useful for therapeutic, diagnostic or industrial

PT purposes, comprises a nanomachine genome encoding a gene set for

PT viability or replication.

XX

PS Example 1; Page 231-240; 250pp; English.

XX

XX The present invention describes a basic genetic operating system for an

CC autonomous prototrophic or autotrophic nanomachine comprising a

CC nanomachine genome encoding a minimal gene set sufficient for viability

CC or replication, optionally in the presence of an autotrophic molecule.

CC Also described is an autonomous prototrophic or autotrophic nanomachine

CC comprising a basic genetic operating system for autonomous prototrophic

CC or autotrophic viability or replication, optionally in the presence of an

CC autotrophic molecule, and a particle envelope. The nanomachines can be

CC used in gene therapy. The basic genetic operating system or nanomachine

CC is useful in therapeutic, diagnostic and industrial applications, e.g. as

FT	exon	/cons_splice= (5'site:YES,3'site:NO) 65149..65277 /*tag= p /number= 2 65278..66763 /*tag= q /number= 2 66764..66820 /*tag= r /number= 3 66821..68117 /*tag= s /number= 3 68118..68270 /*tag= t /number= 4 68271..82001 /*tag= u /number= 4 82002..82109 /*tag= v /number= 5 91488..101286 /*tag= x /product= "MS4A12" /note= "Contains 5 introns" 91488..91760 /*tag= y /number= 1 91761..95209 /*tag= z /number= 1 95210..95347 /*tag= aa /number= 2 95348..96147 /*tag= ab /number= 2 96148..96204 /*tag= ac /number= 3 96205..97864 /*tag= ad /number= 3 97865..97981 /*tag= ae /number= 4 97982..100889 /*tag= af /number= 4 /cons_splice= (5'site:YES,3'site:NO) 100890..101000 /*tag= ag /number= 5 101001..101181 /*tag= ah /number= 5 101182..101283 /*tag= ai /number= 6
XX		
PN	WO200262946-A2.	
XX		
PD	15-AUG-2002.	
XX		
PF	10-DEC-2001; 2001WO-US048437.	
XX		
XX	08-DEC-2000; 2000US-0254362P.	
PR	20-FEB-2001; 2001US-0270057F.	
XX		
XX	(UYDU-) UNIV DUKE.	
PA		
XX		
P1	Tedder TF, Liang YH;	

XX	WPI; 2002-657530/70.
DR	P-PSDB; ABP65025, ABP65029, ABP65045.
XX	
PT	New membrane spanning 4-domain A (MS4A) genes and polypeptides, useful
PT	for generating animal models of atopic disorders, for drug screening, or
PT	for treating (non-) Hodgkin's lymphoma, or allergenic or atopic disorders
XX	in e.g. humans.
XX	
PS	Claim 18; Page 328-385; 450pp; English.
XX	
CC	The invention relates to novel membrane spanning 4-domain A (MS4A)
CC	nucleic acid and polypeptide molecules, comprising human and mouse MS4A.
CC	The polypeptides of the invention have cytotaxtic and anti-allergic
CC	activity. The polynucleotides may have a use in gene therapy. The MS4A
CC	nucleic acids and polypeptides are useful for generating animals (e.g.
CC	mouse) models of atopic disorders, or for drug discovery screens. These
CC	are also useful for treating (non-)Hodgkin's lymphoma, allergic
CC	diseases, atopic disorders or other MS4A-related conditions. The present
CC	sequence represents a human MS4A genomic region, encoding the MS4A7,
CC	MS4A5 and MS4A12 proteins
XX	
SQ	Sequence 104644 BP; 33140 A; 20880 C; 20558 G; 29988 T; 0 U; 78 Other;
	Query Match 21.9%; Score 30.4; DB 6; Length 104644;
	Best Local Similarity 53.3%; Pred. No. 29;
	Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
OY	16 GAACCTTAATAATGCCTGCTCACCGCTCTTTTCTTCAGAAAGGGTGACTATTGTCTG 75
Dd	88420 GAACCCAGATTATTCATGGCTAGGTCTATAGTATTAGACTCAGAATACATTTTTTACUG 88361
OY	76 GTTTATTAACTGTTTATCCCCAAGCAACOATATCAACGCTAGACTGTTCATTGTAAA 135
Dd	88360 GGTCAGAGTTCGTGTTTTTAAAGAAGGAATTAAGACAGACAGCCAGCCAGTCTCATCTTTA 88301

RESULT 18					
ADBI2064_03/c					
Continuation (4 of 18) of ADBI2064 from base 300001 (Alloicoccus otitis entire					
WP Sequence split into 18 fragments LOCUS ADBI2064 Accession ADBI2064					
WP	Fragment Name	Begin	End		
WP	ADBI2064_00	1	110000		
WP	ADBI2064_01	100001	210000		
WP	ADBI2064_02	200001	310000		
WP	ADBI2064_03	300001	410000		
WP	ADBI2064_04	400001	510000		
WP	ADBI2064_05	500001	610000		
WP	ADBI2064_06	600001	710000		
WP	ADBI2064_07	700001	810000		
WP	ADBI2064_08	800001	910000		
WP	ADBI2064_09	900001	1010000		
WP	ADBI2064_10	1000001	1110000		
WP	ADBI2064_11	1100001	1210000		
WP	ADBI2064_12	1200001	1310000		
WP	ADBI2064_13	1300001	1410000		
WP	ADBI2064_14	1400001	1510000		
WP	ADBI2064_15	1500001	1610000		
WP	ADBI2064_16	1600001	1710000		
WP	ADBI2064_17	1700001	1754382		

	Query Match	21.7%	Score 30.2;	DB 9;	Length 110000;
	Best Local Similarity	51.1%;	Pred. No. 34;	Mismatches	0; Gaps 0;
	Matches	71;	Conservative	0;	Mismatches 68; Indels 0;
Qy	1	GTGACTCTGGTCGACGAACCTTAAATTAAGCCCTGCCTCA	CCCCCTCTTTCTTGAGAAAGAGG	60	
Dd	57300	GTAATTTTTCTCGAACCAACTTAAGTTATTTCGAGAATGATCATCTATTTTCTCAA	CTGTA	57241	
Qy	61	GTGACTATTGTCTGGTTTATTAACTGTTTATCCC	AAGCACCATAATCAACGCTAGAC	120	
Dd	57240	ACACTAAATTTTAAAATTAACATATGTTTCGATGTCTCCCATATTTCCCAAACTACA	A	57181	

Qy 121 TGTCTTATTTGTTACACA 139
 Db 57180 CCAGCTAACTGTTTAAACA 57162

RESULT 19

ADJ38283
 ID ADJ38283 standard; cDNA; 622 BP.

XX AC ADJ38283;

XX 06-MAY-2004 (first entry)

XX Plastid division-related Arc6 orthologue cDNA 64.

XX prokaryotic type; plastid division; Ftn2; ARC6; ARC5; Fzo; plant cell;
 KW agronomic; horticultural; crop plant; ornamental plant; woody plant;
 KW herbicide target; gene; ss.

OS Prunus persica.

PN WO2004001003-A2.

XX 31-DEC-2003.

XX 20-JUN-2003; 2003WO-US019536.

XX 20-JUN-2002; 2002US-0390140P.

PR 09-AUG-2002; 2002US-0402242P.

PR 20-JUN-2003; 2003US-00600070.

XX (UNMS) UNIV MICHIGAN STATE.

XX Oosteryoung KW, Vitha S, Koksharova OA, Gao H;

XX WPI; 2004-082486/08.

XX New isolated Ftn2, ARC5 and/or Fzo-like nucleic acid sequences, useful
 PT for further characterizing plastid division in plant cells, and in
 PT varying agronomic and horticultural characteristics of economically
 PT important plants.

XX Disclosure; Fig 26; 287pp; English.

XX This invention relates to novel prokaryotic type or plastid division and
 CC related genes and proteins. In particular, the invention relates to novel
 CC Ftn2 (ARC6), ARC5 and Fzo-like genes and polypeptides. The methods and
 CC compositions of the present invention are useful for further
 CC characterizing plastid division in plant cells, in order to vary
 CC agronomic and horticultural characteristics of economically important
 CC plants, such as crop, ornamental and woody plants. They can also be used
 CC as herbicide targets. The present sequence is a cDNA sequence which is
 CC related to the invention.

XX Sequence 622 BP; 168 A; 125 C; 147 G; 181 T; 0 U; 1 Other;

Query Match 21.6%; Score 30; DB 12; Length 622;
 Best Local Similarity 72.2%; Pred. No. 9.1;
 Matches 39; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 23 AATAATGCTGCTACCCCTCTTTCTTCAGAAAGGGTGACTATTGTCGG 76
 Db 262 ATTACTTCCTATATCATGCTCTCTCTCAGAAAGATGGTGAGTATTAAAGTGG 315

RESULT 20

AAK74790/C
 ID AAK74790 standard; DNA; 10711 BP.

XX AAK74790;

XX 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29602.
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX Homo sapiens.
 OS
 XX WO200157182-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US001354.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.


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PR 15-JAN-1999; 99US-00232149.
PR 15-JAN-1999; 99US-00232880.
PR 09-APR-1999; 99US-00288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX
XX WPI; 2000-171268/15.
XX
XX New polypeptide useful for treating and diagnosing prostate cancer
XX comprises an immunogenic portion of prostate tumor protein.
XX
XX Claim 1; Page 194; 263pp; English.
XX
XX The present invention describes isolated polypeptides, comprising an
XX immunogenic portion of a prostate tumor protein (PTP). The polypeptides
XX and polynucleotides encoding them have cytostatic activity and can be
XX used in vaccines and in gene therapy. The polypeptides and
XX polynucleotides encoding them, antigen presenting cells which express the
XX polypeptides, antibodies against the polypeptides and vaccines comprising
XX them can be used for inhibiting the development of prostate cancer in a
XX patient. The polypeptides can be used to generate antibodies or anti-
XX idiotypic antibodies for passive immuno therapy. A portion of the
XX polynucleotides encoding the polypeptides can be used as a probe or to
XX modulate the expression of the polypeptides. AAH06241 to AAH06691 and
XX AAH92000 to AAH92020 represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;
XX
XX Query Match 21.4%; Score 29.8; DB 3; Length 301;
XX Best Local Similarity 56.7%; Pred. No. 8.6;
XX Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX
XX QY 43 CTTTCTTCAGAAAGGCTGACTATTCTCTGTTTATTAAGTATCCCAAGCA 102
XX |||||
XX Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTGTGTAGTCACTTCTGATTCTGCAATC 89
XX
XX QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
XX |||||
XX Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTTAAACACA 126
XX
XX RESULT 22
XX AAH93642
XX ID AAH93642 standard; cDNA; 301 BP.
XX
XX AC AAH93642;
XX
XX DT 04-OCT-2001 (first entry)
XX
XX DE Human prostate-specific cDNA sequence P808.
XX
XX KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytostatic; gene therapy; metastasis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200151633-A2.
XX
XX PD 19-JUL-2001.
XX
XX PF 16-JAN-2001; 2001WO-US001574.
XX
XX PR 14-JAN-2000; 2000US-00483672.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX Wang A, Meagher MJ;
XX
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```
DR WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.
XX
XX Claim 1; Page 320; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate
XX volume. AAH93357 to AAH93944 and AAH0115 to AAH01318 represent
XX polynucleotide and amino acid sequences used in the exemplification of
XX the present invention
XX
XX Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;
XX
XX Query Match 21.4%; Score 29.8; DB 4; Length 301;
XX Best Local Similarity 56.7%; Pred. No. 8.6;
XX Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX
XX QY 43 CTTTCTTCAGAAAGGCTGACTATTCTCTGTTTATTAAGTATCCCAAGCA 102
XX |||||
XX Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTGTGTAGTCACTTCTGATTCTGCAATC 89
XX
XX QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
XX |||||
XX Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTTAAACACA 126
XX
XX RESULT 23
XX AAS63734
XX ID AAS63734 standard; cDNA; 301 BP.
XX
XX AC AAS63734;
XX
XX DT 29-JAN-2002 (first entry)
XX
XX DE Human prostate cDNA sequence #286.
XX
XX KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
XX OS Homo sapiens.
XX
XX PN WO200173032-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-US009919.
XX
XX PR 27-MAR-2000; 2000US-00536857.
XX PR 09-MAY-2000; 2000US-00568100.
XX PR 12-MAY-2000; 2000US-00570737.
XX PR 13-JUN-2000; 2000US-00593793.
XX PR 17-JUN-2000; 2000US-00605783.
XX PR 09-AUG-2000; 2000US-00636215.
XX PR 29-AUG-2000; 2000US-00651236.
XX PR 06-SEP-2000; 2000US-00657279.
XX PR 02-OCT-2000; 2000US-00679426.
XX PR 10-OCT-2000; 2000US-00685166.
XX PR 09-NOV-2000; 2000US-00709729.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX
```


CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
CC Prostate specific antigen (PSA) P501s was located on chromosome 1.
CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
CC and polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTCTGCTTTATTAAGTGTATCCCAAGCA 102
DB 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
DB 90 ATCAATCAATGCGCTAGAGCACTGACTGTTAACACA 126

RESULT 26
ACA59543
ID ACA59543 standard; cDNA; 301 BP.
XX ACA59543;
XX
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #286.
XX
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
XX 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKET/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX WPI; 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
XX Example 5; SEQ ID NO 293; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 5; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTCTGCTTTATTAAGTGTATCCCAAGCA 102
DB 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
DB 90 ATCAATCAATGCGCTAGAGCACTGACTGTTAACACA 126

RESULT 27
ABL95106
ID ABL95106 standard; cDNA; 301 BP.
XX
AC ABL95106;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P8D8 cDNA sequence SEQ ID NO 293.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX US2002022248-A1.
PN
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.

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PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX (XUJ3/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
PS Claim 1; SEQ ID NO 293; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match      21.4%; Score 29.8; DB 6; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGGTGACTATTCTCTGGTTTATTAAGTGTATCCCAAGCA 102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTGTGTAGTCACTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 AATCAATCAATGGCCTAGAGCACTGACTGTTAAACACA 126

RESULT 28
ACC95270
ID ACC95270 standard; cDNA; 301 BP.
XX
XX ACC95270;
AC ACC95270;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 293.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX

OS Homo sapiens.
XX
PN WQ200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolisC, Foy TM, Watanabe Y;
PI Deng T;
XX
DR WPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 5; Page 388; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match      21.4%; Score 29.8; DB 8; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGGTGACTATTCTCTGGTTTATTAAGTGTATCCCAAGCA 102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTGTGTAGTCACTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 AATCAATCAATGGCCTAGAGCACTGACTGTTAAACACA 126

RESULT 29
ADBI3743
ID ADBI3743 standard; cDNA; 301 BP.
XX
XX ADBI3743;
AC ADBI3743;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific cDNA JF8D8.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.

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XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00638215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
XX response, or for treating or diagnosis cancer, preferably prostate
XX cancer.
XX
XX Example 5; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
XX 11-542 amino acids of ADB13563 comprising a sequence ADB1487. The
XX peptides comprise a fragment ADB13563 of that contain naturally processed
XX T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX alleles. ADB13563 is a polypeptide encoded by a human prostate specific
XX cDNA, one of 648 disclosed as new. Also included are nucleic acids
XX encoding the proteins and peptides, expression vectors, a host cell
XX transformed with the vector, an isolated antibody (or antigen binding
XX fragment) that specifically binds to the protein or peptide, detecting
XX the presence of a cancer in a patient (comprising contacting a patient
XX sample with a binding agent that binds to the peptides or a polypeptide
XX appearing as ADB13558, detecting the amount of polypeptide that binds to
XX the agent and comparing the amount of polypeptide to a predetermined cut-
XX off value to determine the presence of cancer), a fusion protein
XX comprising the peptides or proteins, stimulating or expanding T cells
XX specific for a tumour protein comprising contacting T cells with the
XX peptides or the isolated T cell population, treating prostate cancer in a
XX patient comprising administering a composition comprising the peptides,
XX nucleic acids, antibodies or compounds, determining the presence of a
XX cancer in a patient and treating prostate cancer in a patient comprising
XX incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
XX from a patient with the peptides or antigen presenting cells that express
XX the peptides so that the T cells proliferate, and administering the
XX proliferated T cells to the patient. The peptides (or an oligonucleotide
XX that hybridises to nucleic acid encoding them), is used to detect the
XX presence of cancer in a patient. The peptides, nucleic acids encoding, or
XX antigen-presenting cells expressing the nucleic acid, are used to
XX stimulate or expand T cells specific for a tumour protein. The peptides,
XX nucleic acids, antibodies, fusion proteins, T cell populations or antigen
XX presenting cells are used to stimulate an immune response or treat

CC prostate cancer in a patient. The present sequence is one of the
CC disclosed human prostate specific cDNAs. Note: Except where otherwise
CC indicated, the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
XX Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;
SQ
Query Match 21.4%; Score 29.8; DB 10; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 43 CTTTCTTCAGAAAGGGTGACTATTCTGCTTTATTAAGTCTTATCCCAAGCA 102
DB 30 CTGTTCTCACTGAAAAGTGGCTAATGCTGTGTAGTCACTCTGATTCTGACAATC 89
QY 103 CCATATCAACGCTAGACTGTCTTATTGTTAAACACA 139
DB 90 AATCATCAATGGCTAGAGCACTGACTGTTTAAACACA 126
RESULT 30
ID ADG26159 standard; cDNA; 301 BP.
XX
AC ADG26159;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human prostate-specific cDNA #286.
XX
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KW cytostatic.
XX
OS Homo sapiens.
XX
XX US2003157089-A1.
XX
PD 21-AUG-2003.
XX
XX 09-MAY-2002; 2002US-00144678.
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 29-AUG-2000; 2000US-00638215.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS;
PI Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Haral J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX WPI; 2003-777973/73.
DR
XX
XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 5; SEQ ID NO 293; 99pp; English.
XX
XX The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 301 BP; 83 A; 73 C; 60 G; 85 T; 0 U; 0 Other;

Query Match 21.4%; Score 29.8; DB 10; Length 301;
Best Local Similarity 56.7%; Pred. No. 8.6;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGGTGACTATTGCTCGTTTATTAACTGTTATCCCAAGCA 102
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
30 CTGTTCTCACTGMAAAGTCGGCTAATGCTCTTGTTAGTCACTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
90 AATCAATCAATGCGCTAGAGCACTGACTGTTAACACA 126

Search completed: December 22, 2004, 02:36:23
Job time : 1042 secs

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 03:01:57 ; Search time 266 Seconds

(without alignments)

2884.949 Million cell updates/sec

Title: US-10-070-882A-2

Perfect score: 139

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Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.2	26.8	1385	16	US-10-282-122A-37352
2	31	22.3	772	17	US-10-363-829-150
3	31	22.3	810	17	US-10-363-829-237
4	30.6	22.0	2799	9	US-09-738-626-2992
5	30.6	22.0	3309400	9	US-09-738-626-1
6	30.4	21.9	31241	10	US-09-960-870-13
7	30.4	21.9	31241	10	US-09-960-858-13
8	30.4	21.9	31241	16	US-10-251-668-13
9	30.4	21.9	104644	17	US-10-433-287-79
10	30.4	21.9	109559	17	US-10-322-281-137
11	30.2	21.7	138363	17	US-10-367-094-117
12	30	21.6	458	16	US-10-424-599-105245

13	21.6	30	622	17	US-10-600-070-201	Sequence 201, App
14	21.4	29.8	301	9	US-09-759-143-293	Sequence 293, App
15	29.8	21.4	301	9	US-09-780-669-293	Sequence 293, App
16	29.8	21.4	301	9	US-09-822-827-293	Sequence 293, App
17	29.8	21.4	301	9	US-09-232-880-293	Sequence 293, App
18	29.8	21.4	301	9	US-09-895-793-293	Sequence 293, App
19	29.8	21.4	301	9	US-09-895-814-293	Sequence 293, App
20	29.8	21.4	301	13	US-10-012-896-293	Sequence 293, App
21	29.8	21.4	301	14	US-10-010-940-293	Sequence 293, App
22	29.8	21.4	301	15	US-10-144-678A-293	Sequence 293, App
23	29.8	21.4	301	15	US-10-294-025-293	Sequence 293, App
24	29.8	21.4	434	15	US-10-102-524-307	Sequence 307, App
25	29.8	21.4	434	15	US-10-102-524-540	Sequence 540, App
26	29.8	21.4	444	13	US-10-027-632-81146	Sequence 81146, A
27	29.8	21.4	444	15	US-10-027-632-81146	Sequence 81146, A
28	29.8	21.4	463	13	US-10-027-632-109769	Sequence 109769, App
29	29.8	21.4	463	15	US-10-027-632-109769	Sequence 109769, App
30	29.8	21.4	492	9	US-09-954-456-46	Sequence 46, Appl
31	29.8	21.4	492	9	US-09-954-456-962	Sequence 962, Appl
32	29.8	21.4	617	13	US-10-027-632-229999	Sequence 229999, App
33	29.8	21.4	617	15	US-10-027-632-229999	Sequence 229999, App
34	29.8	21.4	1448	16	US-10-131-487A-46	Sequence 46, Appl
35	29.8	21.4	2962	15	US-10-104-047-1343	Sequence 1343, App
36	29.8	21.4	3042	15	US-10-205-823-155	Sequence 155, App
37	29.8	21.4	3042	15	US-10-177-293-183	Sequence 183, App
38	29.8	21.4	3042	15	US-10-210-120-114	Sequence 114, App
39	29.8	21.4	3042	15	US-10-341-434-120	Sequence 120, App
40	29.8	21.4	3042	15	US-10-172-118-1654	Sequence 1654, App
41	29.8	21.4	3042	16	US-10-342-887-1654	Sequence 1654, App
42	29.8	21.4	3154	17	US-10-115-635-360	Sequence 360, App
43	29.8	21.4	3174	16	US-10-351-334-86	Sequence 86, Appl
44	29.6	21.3	611	13	US-10-027-632-197263	Sequence 197263, App
45	29.6	21.3	611	15	US-10-027-632-197263	Sequence 197263, App
46	29.6	21.3	483728	18	US-10-699-156-2	Sequence 2, Appl1
47	29.4	21.2	567	13	US-10-027-632-51360	Sequence 51360, A
48	29.4	21.2	567	15	US-10-027-632-51360	Sequence 51360, A
49	29.4	21.2	592	13	US-10-027-632-61820	Sequence 61820, A
50	29.4	21.2	592	15	US-10-027-632-61820	Sequence 61820, A
51	29.4	21.2	32249	10	US-09-764-891-7477	Sequence 7477, App
52	29.4	21.2	43602	15	US-10-085-959-18	Sequence 18, Appl
53	29.2	21.0	16593	8	US-08-961-527-52	Sequence 52, Appl
54	29.2	21.0	16593	16	US-10-158-844-52	Sequence 52, Appl
55	29	20.9	510	13	US-10-027-632-236290	Sequence 236290, App
56	29	20.9	510	15	US-10-027-632-236290	Sequence 236290, App
57	29	20.9	607	13	US-10-027-632-13067	Sequence 13067, A
58	29	20.9	607	15	US-10-027-632-13067	Sequence 13067, A
59	29	20.9	740	13	US-10-027-632-146426	Sequence 146426, App
60	29	20.9	740	15	US-10-027-632-146426	Sequence 146426, App
61	28.8	20.7	2347	10	US-09-880-573-113	Sequence 113, App
62	28.6	20.6	481	9	US-09-783-590-1098	Sequence 1098, App
63	28.6	20.6	485	9	US-09-864-761-4049	Sequence 4049, App
64	28.6	20.6	500	13	US-10-027-632-80079	Sequence 80079, A
65	28.6	20.6	500	15	US-10-027-632-80079	Sequence 80079, A
66	28.6	20.6	500	15	US-10-027-632-80079	Sequence 80079, A
67	28.6	20.6	500	15	US-10-027-632-301423	Sequence 301423, App
68	28.6	20.6	553	13	US-10-027-632-303134	Sequence 303134, App
69	28.6	20.6	553	15	US-10-027-632-303134	Sequence 303134, App
70	28.6	20.6	573	13	US-10-027-632-67583	Sequence 67583, A
71	28.6	20.6	573	15	US-10-027-632-67583	Sequence 67583, A
72	28.6	20.6	2676	9	US-09-974-592-11	Sequence 11, Appl
73	28.6	20.6	16397	8	US-08-781-986A-205	Sequence 205, App
74	28.6	20.6	16397	16	US-10-329-624-205	Sequence 1561, App
75	28.6	20.6	84926	13	US-10-087-192-1561	Sequence 180415, App
76	28.4	20.4	585	13	US-10-027-632-180415	Sequence 236049, App
77	28.4	20.4	585	15	US-10-027-632-180415	Sequence 236049, App
78	28.4	20.4	615	13	US-10-027-632-236049	Sequence 191479, App
79	28.4	20.4	615	15	US-10-027-632-236049	Sequence 191479, App
80	28.4	20.4	659	13	US-10-027-632-191479	Sequence 1, Appl1
81	28.4	20.4	659	15	US-10-027-632-191479	Sequence 255960, App
82	28.4	20.4	1092	15	US-10-138-701-1	Sequence 255960, App
83	28.4	20.4	1305	13	US-10-027-632-255960	Sequence 391, App
84	28.4	20.4	1305	15	US-10-027-632-255960	
85	28.4	20.4	2407	8	US-08-781-986A-391	

Sequence 391, App
Sequence 46078, A
Sequence 188, App
Sequence 188, App
Sequence 41, Appl
Sequence 195038,
Sequence 195038,
Sequence 36959, A
Sequence 9454, Ap
Sequence 2035, Ap
Sequence 36958, A
Sequence 248955,
Sequence 248955,
Sequence 248956,
Sequence 248956,

ALIGNMENTS

RESULT 1
US-10-282-122A-37352
; Sequence 37352, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37352
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (72)..(72)
; OTHER INFORMATION: n=g, a, t or c
; FEATURE:

NAME/KEY: misc feature
LOCATION: (74)..(75)
OTHER INFORMATION: n=g, a, t or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (158)..(158)
OTHER INFORMATION: n=g, a, t or c
US-10-282-122A-37352
Query Match 26.8%; Score 37.2; DB 16; Length 1385;
Best Local Similarity 92.9%; Pred. No. 0.062;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGACTCTGTCGACGAACTTAATAATGCTGCCTCACCCCT 42
DB 1344 GTGACTCTGTCGACGAACTTAATAATGCTGCCTCACCCCT 1385
RESULT 2
US-10-363-829-150/c
; Sequence 150, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 150
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (72)..(72)
; OTHER INFORMATION: Incyte ID No: LG:994938.1:2000SEP08
; US-10-363-829-150

Query Match 22.3%; Score 31; DB 17; Length 772;
Best Local Similarity 57.9%; Pred. No. 5.9;
Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 45 TTCTTTCCAGAGAGGGTGACTATTGTCTGGTTTATTACTGTTATCCCAAGCACC 104
DB 549 TTCCAATAAAAAAGCTCCATTAGTTTATTTATCAGTGTTCCTCAAAAGCGCT 490

QY 105 ATAATCAAGCTAGACTGTCTTTATTGTTAAACACA 139
DB 489 TTCTGTAATGCTAGAAATCTCTCAGTGTCAACACA 455

RESULT 3

US-10-363-829-237/c
; Sequence 237, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Dafo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 237
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LI:814261.1:2000SEP08

US-10-363-829-237

Query Match 22.3%; Score 31; DB 17; Length 810;
Best Local Similarity 57.9%; Pred. No. 6.1;
Matches 55; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 45 TTCTTTCCAGAGAGGGTGACTATTGTCTGGTTTATTACTGTTATCCCAAGCACC 104
DB 549 TTCCAATAAAAAAGCTCCATTAGTTTATTTATCAGTGTTCCTCAAAAGCGCT 490

QY 105 ATAATCAAGCTAGACTGTCTTTATTGTTAAACACA 139
DB 489 TTCTGTAATGCTAGAAATCTCTCAGTGTCAACACA 455

RESULT 4

US-09-738-626-2992
; Sequence 2992, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO 2992
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2992

Query Match 22.0%; Score 30.6; DB 9; Length 2799;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 AACTTAAATAGCTGCTCACCCTCTTTCTTTCAGAAAGGGTGACTATTGTCGG 76
DB 271 AACGTCATTGATGGCAGCAAGCATGCTTCATGCAAGAAAGACTCAACCAITGGTTGG 330

QY 77 TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGGCTAGACTGTTCTTATTGTT 133
DB 331 ATCATCGACAGTGTCTGTTTCACACCAACCAATTCACCGATCCACGATGATCGGT 387

RESULT 5

US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 22.0%; Score 30.6; DB 9; Length 3309400;
Best Local Similarity 53.8%; Pred. No. 2.6e+02;
Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 17 AACTTAATAATGCTGCTCCCTCACCTCTTTCTTCAGAAAGAGGTGACTATTGTCGG 76
Db 2900056 AAGTCATTGATGGCAGGAGGATGCTTCATGCAGAGAACTCAACCAATGGTGG 2899997
QY 77 TTTATTAACTGTTTATCCCAAGACCAATCAACGCTAGACTGTTCTATTGTT 133
Db 2899996 ATCATGCACAGTCTGTTTACACCAACCAATTCACCGATCCAACTGATGATCGGT 2899940

RESULT 6

US-09-960-870-13/c
; Sequence 13, Application US/09960870
; Publication No. US20030134281A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen
; TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
; FILE REFERENCE: P-EA 4738
; CURRENT APPLICATION NUMBER: US/09/960,870
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31241
; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-870-13

Query Match 21.9%; Score 30.4; DB 10; Length 31241;
Best Local Similarity 55.8%; Pred. No. 45;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 34 CCTCACCTCTTTCTTCAGAAAGAGGTGACTATTGTCGTTTATTAACTGTTATC 93
Db 25866 CCTCAGCAATTTTTTTTAAACCAAGTGGTGTACCATCTGGTTTGTCTCTTGTGC 25807
QY 94 CCCAAAGCACCAATCAACGCTAGACTGTTCTTATTGTTAAACA 137
Db 25806 ATTAAAGAAGCGTATCAAACTATACCCCTTTTTTGTCTAAAA 25763

RESULT 7

US-09-960-858-13/c
; Sequence 13, Application US/09960858
; Publication No. US2003013877A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen
; TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
; FILE REFERENCE: P-EA 4974
; CURRENT APPLICATION NUMBER: US/09/960,858
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31241
; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-858-13

Query Match 21.9%; Score 30.4; DB 10; Length 31241;
Best Local Similarity 55.8%; Pred. No. 45;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 34 CCTCACCTCTTTCTTCAGAAAGAGGTGACTATTGTCGTTTATTAACTGTTATC 93
Db 25866 CCTCAGCAATTTTTTTTAAACCAAGTGGTGTACCATCTGGTTTGTCTCTTGTGC 25807
QY 94 CCCAAAGCACCAATCAACGCTAGACTGTTCTTATTGTTAAACA 137
Db 25806 ATTAAAGAAGCGTATCAAACTATACCCCTTTTTTGTCTAAAA 25763

RESULT 8

US-10-251-668-13/c
; Sequence 13, Application US/10251668
; Publication No. US20040063097A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen
; TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
; FILE REFERENCE: P-EA 5441
; CURRENT APPLICATION NUMBER: US/10/251,668
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/960,607
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31241
; TYPE: DNA
; ORGANISM: M. genitalium
US-10-251-668-13

Query Match 21.9%; Score 30.4; DB 16; Length 31241;
Best Local Similarity 55.8%; Pred. No. 45;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 34 CCTCACCTCTTTCTTCAGAAAGAGGTGACTATTGTCGTTTATTAACTGTTATC 93
Db 25866 CCTCAGCAATTTTTTTTAAACCAAGTGGTGTACCATCTGGTTTGTCTCTTGTGC 25807
QY 94 CCCAAAGCACCAATCAACGCTAGACTGTTCTTATTGTTAAACA 137
Db 25806 ATTAAAGAAGCGTATCAAACTATACCCCTTTTTTGTCTAAAA 25763

RESULT 9

US-10-433-287-79/c
; Sequence 79, Application US/10433287
; Publication No. US20040137566A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; FILE REFERENCE: 180/132 PCT/US
; CURRENT APPLICATION NUMBER: US/10/433,287
; CURRENT FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 79
; LENGTH: 104644
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:

```

; NAME/KEY: genomic DNA
; LOCATION: (1)..(104644)
; OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39)..(39)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143)..(143)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (231)..(231)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (242)..(242)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (362)..(362)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11659)..(11659)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11699)..(11699)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: MS4A7 initial coding_region
; LOCATION: (17493)..(17639)
; FEATURE:
; NAME/KEY: MS4A7 coding_region
; LOCATION: (19439)..(19573)
; FEATURE:
; NAME/KEY: MS4A7 coding_region
; LOCATION: (21068)..(21124)
; FEATURE:
; NAME/KEY: MS4A7 coding_region
; LOCATION: (23741)..(23947)
; FEATURE:
; NAME/KEY: MS4A7 coding_region
; LOCATION: (27037)..(27138)
; FEATURE:
; NAME/KEY: MS4A7 coding_region
; LOCATION: (28139)..(28210)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (32640)..(32640)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: MS4A5 initial coding_region
; LOCATION: (64028)..(64180)
; FEATURE:
; NAME/KEY: MS4A5 coding_region
; LOCATION: (65149)..(65277)
; FEATURE:
; NAME/KEY: MS4A5 coding_region
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; LOCATION: (66764)..(66820)
; FEATURE:
; NAME/KEY: MS4A5 coding_region
; LOCATION: (68118)..(68270)
; FEATURE:
; NAME/KEY: MS4A5 coding_region
; LOCATION: (82002)..(82109)
; FEATURE:
; NAME/KEY: MS4A12 initial coding_region
; LOCATION: (91488)..(91760)
; FEATURE:
; NAME/KEY: MS4A12 coding_region
; LOCATION: (95210)..(95347)
; FEATURE:
; NAME/KEY: MS4A12 coding_region
; LOCATION: (96148)..(96204)
; FEATURE:
; NAME/KEY: MS4A12 coding_region
; LOCATION: (97865)..(97981)
; FEATURE:
; NAME/KEY: MS4A12 coding_region
; LOCATION: (100890)..(101000)
; FEATURE:
; NAME/KEY: MS4A12 coding_region
; LOCATION: (101182)..(101283)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (104561)..(104625)
; OTHER INFORMATION: n is a, c, g, or t
US-10-433-287-79

Query Match      21.9%; Score 30.4; DB 17; Length 104644;
Best Local Similarity 53.3%; Pred. No. 75;
Matches 64; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      16  GAACTTAATAATGCTGCTCACCTCTTTTCTTCAGAAAGGGTGACTATTGCTG 75
Db      88420  GAACCCAGATTATTCATGGCTAGGCTCTATAGTATTAGGACTCAGAAATACATTTTACTG 88361

QY      76  GTTTATTAACTGTTTATCCCAAGCACCATAATCAACGCTAGACTGTGTTATTGTTAA 135
Db      88360  GGTCAAGTCTCGTTTATATAAAGGAATTAAAGACAGACAGCCAGCTTCTGATTTCTTA 88301

RESULT 10
US-10-322-281-137/c
; Sequence 137, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 109559
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(109559)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-137

Query Match      21.9%; Score 30.4; DB 17; Length 109559;
Best Local Similarity 55.8%; Pred. No. 77;
Matches 58; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY      4  ACTCTGTCGAGAACTTAAATAATGCTGCTCACCTCTTTTCTTCAGAAAGGGTG 63
```


Db 8124 AATGCGCCCAAGTTCCGACGAGTGACTCCGTAACATATCGTTTATGAAGAAAAGTCCACG 8065

QY 64 ACTATTGTCTGGTTTATTAACTGTTTATCCCAAGCACCAATA 107

Db 8064 ACTTCTGTTTGCACATGTTCTGTGTCTCCACAGCAACATA 8021

RESULT 11

US-10-367-094-117

; Sequence 117, Application US/10367094

; Publication No. US20040170982A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer

; FILE REFERENCE: 529452001500

; CURRENT APPLICATION NUMBER: US/10/367,094

; CURRENT FILING DATE: 2003-02-14

; NUMBER OF SEQ ID NOS: 203

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 117

; LENGTH: 138363

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(138363)

; OTHER INFORMATION: n = A, T, C or G

US-10-367-094-117

Query Match 21.7%; Score 30.2; DB 17; Length 138363;

Best Local Similarity 56.6%; Pred. No. 99;

Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 39 CCTCTTTTCTTCAGAAAGGAGTGACTATTGTCGTGTTTATTAAGTATCCCA 98

Db 131756 CTCTCTTTCTTTTATTAGTCTAGTAGCCCTATTTTTATTAATTTTTC 131815

QY 99 AGCACCAATATCAACGCTAGACTGTTCTTATTCTTAACA 137

Db 131816 ATCCAGCTCTGATTCATGATCITTTGATTTTTC 131854

RESULT 12

US-10-424-599-105245/c

; Sequence 105245, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 105245

; LENGTH: 458

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(458)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_66052C.1

US-10-424-599-105245

Query Match

Best Local Similarity 21.6%; Score 30; DB 16; Length 458;

Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 11 TCAGCAACTTAAATAATGCTCGCTCACCCCTCTTTCTTCAGAAAGGAGTCACTATT 70

Db 193 TCAGGGCCCTCAATTTATGATGATGATCTAGTTCATTTTATGTAAGATGAAGAGTCCC 134

QY 71 GTCTGGTTTATTAACTGTTTATCCCAAGACACCATATAATCAACGGCTAGAC 120

Db 133 GTCACGATTATCATTTTTTAAATATGTAAGCTCCCTTGTCAACATTGAC 84

RESULT 13

US-10-600-070-201

; Sequence 201, Application US/10600070

; Publication No. US20040139500A1

; GENERAL INFORMATION:

; APPLICANT: Osteryoung, Katherine W.

; APPLICANT: Witka, Stanislaw

; APPLICANT: Koksharova, Olga A.

; APPLICANT: Gao, Hong

; TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of

; FILE REFERENCE: MSU-08153

; CURRENT APPLICATION NUMBER: US/10/600,070

; CURRENT FILING DATE: 2003-06-20

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 201

; LENGTH: 622

; TYPE: DNA

; ORGANISM: Prunus persica

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (609)..(609)

; OTHER INFORMATION: n is a, c, g, or t

US-10-600-070-201

Query Match

Best Local Similarity 21.6%; Score 30; DB 17; Length 622;

Matches 39; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 23 AATAATGCTGCTCACCCCTCTTTCTTCAGAAAGGAGTCACTATTGTCG 76

Db 262 ATTACTTCTATATCATGCTATCTTCTTCAGAAAGATGCTGATTTAAGTGG 315

RESULT 14

US-09-759-143-293

; Sequence 293, Application US/09759143

; Patent No. US200202248A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121-427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-293

Query Match          21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGCTGACTATTGCTGGTTTAACTGTTTATCCCAAAGCA 102
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGCTAGTCACTTCTGATTCTGCAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 15
US-09-780-669-293
; Sequence 293, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-293

Query Match          21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGCTGACTATTGCTGGTTTAACTGTTTATCCCAAAGCA 102
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGCTAGTCACTTCTGATTCTGCAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 16
US-09-822-827-293
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```
; Sequence 293, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-293

Query Match          21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGCTGACTATTGCTGGTTTAACTGTTTATCCCAAAGCA 102
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGCTAGTCACTTCTGATTCTGCAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 17
US-09-232-880-293
; Sequence 293, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-880-293

Query Match          21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGAGGCTGACTATTGCTGGTTTAACTGTTTATCCCAAAGCA 102
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGCTAGTCACTTCTGATTCTGCAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 18
US-09-895-793-293
; Sequence 293, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
```

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; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-293

Query Match      21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
    |||||
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
    |||||
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 19
US-09-895-814-293
; Sequence 293, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-293

Query Match      21.4%; Score 29.8; DB 13; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
    |||||
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
    |||||
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 19
US-09-895-814-293
; Sequence 293, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
```

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; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-293

Query Match      21.4%; Score 29.8; DB 9; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
    |||||
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
    |||||
Db 90 AATCAATCAATGCGCTAGAGCACTGACTGTTAAACACA 126

RESULT 20
US-10-012-896-293
; Sequence 293, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-293

Query Match      21.4%; Score 29.8; DB 13; Length 301;
Best Local Similarity 56.7%; Pred. No. 10;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
    |||||
Db 30 CTGTTCTCACTGAAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGATTCTGACAATC 89
```

Qy	103	CCATATCAACGCTAGACTGTTCCTTATTGTTAAACACA	139
Db	90	AATCAATCAATGGCCTAGAGCACTGACTGTGTTAAACACA	126
RESULT 21			
US-10-010-940-293			
; Sequence 293, Application US/10010940			
; Publication No. US200308062A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan Louise			
; APPLICANT: Jiang Yuqi			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Kalos, Michael			
; APPLICANT: Fanger, Gary			
; APPLICANT: Retter, Mark			
; APPLICANT: Solk, John			
; APPLICANT: Day, Craig			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
; FILE REFERENCE: 210121.427D3			
; CURRENT APPLICATION NUMBER: US/10/010,940			
; CURRENT FILING DATE: 2001-12-05			
; NUMBER OF SEQ ID NOS: 575			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 293			
; LENGTH: 301			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-10-010-940-293			
Query Match 21.4%; Score 29.8; DB 14; Length 301;			
Best Local Similarity 56.7%; Pred. No. 10;			
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;			
Qy	43	CTTTCTTCAGAAAGGCTGACTATTGCTCGTGTTTAACTGTTATCCCCAAAGCA	102
Db	30	CTGTTCTCACTGAAAAGTCTGCCTAAATGCTCTGTGTAGTCACCTTCTGATTCGACAATC	89
Qy	103	CCATATCAACGCTAGACTGTTCCTTATTGTTAAACACA	139
Db	90	AATCAATCAATGGCCTAGAGCACTGACTGTGTTAAACACA	126
RESULT 22			
US-10-144-678A-293			
; Sequence 293, Application US/10144678A			
; Publication No. US200301570B9A1			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yugu			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Solk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
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; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
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; APPLICANT: Wang, Aijun			
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; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
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; APPLICANT: Wang, Aijun			
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; APPLICANT: Hepler, William T.			
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; APPLICANT: Day, Craig H.			
; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
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; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
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; APPLICANT: Vedvick, Thomas S.			
; APPLICANT: Carter, Darriek			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A. W.			
; APPLICANT: Hepler, William T.			
; APPLICANT: Hural, John			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			

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/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ FILE REFERENCE: 210121.572
/ CURRENT APPLICATION NUMBER: US/10/102,524
/ CURRENT FILING DATE: 2002-03-19
/ NUMBER OF SEQ ID NOS: 1863
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 307
/ LENGTH: 434
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 44, 177, 178
/ OTHER INFORMATION: n = A,T,C or G
US-10-102-524-307

Query Match      21.4%; Score 29.8; DB 15; Length 434;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
Db 271 CTGTTCTCACTGAAAGTCTGGCTAAATGCTCTTGTGTAGTCACTTCTGATTCTGCAATC 330

QY 103 CCATAATCAACGGCTAGACTGTTCTTATTGTTAAACACA 139
Db 331 AATCAATCAATGCGCTAGACACTGACTGTTAAACACA 367

RESULT 25
US-10-102-524-540
/ Sequence 540, Application US/10102524
/ Publication No. US20030109434A1
/ GENERAL INFORMATION:
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Gordon, Brian
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ FILE REFERENCE: 210121.572
/ CURRENT APPLICATION NUMBER: US/10/102,524
/ CURRENT FILING DATE: 2002-03-19
/ NUMBER OF SEQ ID NOS: 1863
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 540
/ LENGTH: 434
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-102-524-540

Query Match      21.4%; Score 29.8; DB 15; Length 434;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCA 102
Db 271 CTGTTCTCACTGAAAGTCTGGCTAAATGCTCTTGTGTAGTCACTTCTGATTCTGCAATC 330

QY 103 CCATAATCAACGGCTAGACTGTTCTTATTGTTAAACACA 139
Db 331 AATCAATCAATGCGCTAGACACTGACTGTTAAACACA 367

RESULT 26
US-10-027-632-81146
/ Sequence 81146, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
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/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 81146
/ LENGTH: 444
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-81146

Query Match      21.4%; Score 29.8; DB 13; Length 444;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 31 CTGCTCCACCCCTCTTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTATTAACCTGTTT 90
Db 318 GAGCTTCACTCTTGCTTACATATAGGCTGCTGGCTGCTTTTCATGCTACACACTGTTT 377

QY 91 ATCCCAAGCACCAATAATCAACGGCTAGACTGTTCTT 127
Db 378 ATCCCAAGGCGCTAAATATATATCTATCCAGATTTT 414

RESULT 27
US-10-027-632-81146
/ Sequence 81146, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 81146
/ LENGTH: 444
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-81146
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Query Match      21.4%; Score 29.8; DB 15; Length 444;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 31 CTGCCTCACCTCTTTTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTT 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 318 CAGCTTCACCTCTTGCTTACATATAAGGCTGTGGCTGCTTTCATGCTACAACTGTTT 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 91 ATCCCAAGACCATTAATCAACGCTAGACTGTTCCT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 378 ATCCCAAGACGCTAAATAATATATACTATCCAGATTTT 414
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RESULT 28
US-10-027-632-109769
; Sequence 109769, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109769
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-109769

Query Match      21.4%; Score 29.8; DB 13; Length 463;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 31 CTGCCTCACCTCTTTTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTT 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 CAGCTTCACCTCTTGCTTACATATAAGGCTGTGGCTGCTTTCATGCTACAACTGTTT 425
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QY 91 ATCCCAAGACCATTAATCAACGCTAGACTGTTCCT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 ATCCCAAGACGCTAAATAATATATACTATCCAGATTTT 462
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RESULT 29
US-10-027-632-109769
; Sequence 109769, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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Query Match      21.4%; Score 29.8; DB 15; Length 463;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 31 CTGCCTCACCTCTTTTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTT 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 CAGCTTCACCTCTTGCTTACATATAAGGCTGTGGCTGCTTTCATGCTACAACTGTTT 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 91 ATCCCAAGACCATTAATCAACGCTAGACTGTTCCT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 ATCCCAAGACGCTAAATAATATATACTATCCAGATTTT 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 30
US-09-954-456-46
; Sequence 46, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-46
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Query Match      21.4%; Score 29.8; DB 9; Length 492;
Best Local Similarity 56.7%; Pred. No. 12;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 43 CTTTCTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTGTTTATCCCAAAGCA 102
Db    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 77 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTGTAGTCACTTCTGTGATTCTGACAATC 136
Db    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
Db    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 137 AATCAATCAATGGCTAGAGCACTGACTGTGTTAAACACA 173
Db    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: December 22, 2004, 04:21:54
Job time : 496 secs

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 01:50:26 ; Search time 66 Seconds
(without alignments)
1496.964 Million cell updates/sec

Title: US-10-070-882A-2
Perfect score: 139
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Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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5: /cgn2_6/prodata/1/ina/PCUS COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfileseq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	29.8	21.4	301	3	US-09-439-213-293
2	29.8	21.4	301	3	US-09-352-616A-293
3	29.8	21.4	301	4	US-09-232-149A-293
4	29.8	21.4	301	4	US-09-159-812-293
5	29.8	21.4	301	4	US-09-636-215-293
6	29.8	21.4	301	4	US-09-685-166A-293
7	29.8	21.4	301	4	US-09-688-489-293
8	29.8	21.4	301	4	US-09-679-426-293
9	29.8	21.4	1143	4	US-09-107-532A-1865
10	29.8	21.4	2143	4	US-09-673-395A-82
11	29.8	21.4	3174	4	US-09-489-847-86
12	29.2	21.0	16593	4	US-08-961-527-52
13	29.0	20.9	3010	3	US-08-714-918-71
14	29.0	20.9	3010	3	US-09-265-315-71
15	29.0	20.9	3010	3	US-09-265-315-71
16	29.0	20.9	3010	3	US-09-266-417-71
17	29.0	20.9	3010	4	US-09-528-709-71
18	29.0	20.9	3010	4	US-09-527-745-71
19	28.8	20.7	2347	1	US-08-453-695A-113
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21	28.8	20.7	2347	2	US-08-453-702A-113
22	28.8	20.7	2347	3	US-09-099-639-113
23	28.8	20.7	2347	5	PCT-US95-08071-113
24	28.6	20.6	2676	3	US-09-212-971-11
25	28.6	20.6	2676	3	US-08-800-929A-11
26	28.6	20.6	2676	3	US-09-617-053A-11
27	28.6	20.6	16397	4	US-08-956-171E-205
28	28.6	20.6	16397	4	US-08-956-171E-205
29	28.6	20.6	16397	4	US-08-956-171E-205
30	28.6	20.6	16397	4	US-08-956-171E-205
31	28.6	20.6	16397	4	US-08-956-171E-205
32	28.6	20.6	16397	4	US-08-956-171E-205
33	28.6	20.6	16397	4	US-08-956-171E-205
34	28.6	20.6	16397	4	US-08-956-171E-205
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41	28.6	20.6	16397	4	US-08-956-171E-205
42	28.6	20.6	16397	4	US-08-956-171E-205
43	28.6	20.6	16397	4	US-08-956-171E-205
44	28.6	20.6	16397	4	US-08-956-171E-205
45	28.6	20.6	16397	4	US-08-956-171E-205
46	28.6	20.6	16397	4	US-08-956-171E-205
47	28.6	20.6	16397	4	US-08-956-171E-205
48	28.6	20.6	16397	4	US-08-956-171E-205
49	28.6	20.6	16397	4	US-08-956-171E-205
50	28.6	20.6	16397	4	US-08-956-171E-205
51	28.6	20.6	16397	4	US-08-956-171E-205
52	28.6	20.6	16397	4	US-08-956-171E-205
53	28.6	20.6	16397	4	US-08-956-171E-205
54	28.6	20.6	16397	4	US-08-956-171E-205
55	28.6	20.6	16397	4	US-08-956-171E-205
56	28.6	20.6	16397	4	US-08-956-171E-205
57	28.6	20.6	16397	4	US-08-956-171E-205
58	28.6	20.6	16397	4	US-08-956-171E-205
59	28.6	20.6	16397	4	US-08-956-171E-205
60	28.6	20.6	16397	4	US-08-956-171E-205
61	28.6	20.6	16397	4	US-08-956-171E-205
62	28.6	20.6	16397	4	US-08-956-171E-205
63	28.6	20.6	16397	4	US-08-956-171E-205
64	28.6	20.6	16397	4	US-08-956-171E-205
65	28.6	20.6	16397	4	US-08-956-171E-205
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88	28.6	20.6	16397	4	US-08-956-171E-205
89	28.6	20.6	16397	4	US-08-956-171E-205
90	28.6	20.6	16397	4	US-08-956-171E-205
91	28.6	20.6	16397	4	US-08-956-171E-205
92	28.6	20.6	16397	4	US-08-956-171E-205
93	28.6	20.6	16397	4	US-08-956-171E-205
94	28.6	20.6	16397	4	US-08-956-171E-205
95	28.6	20.6	16397	4	US-08-956-171E-205
96	28.6	20.6	16397	4	US-08-956-171E-205
97	28.6	20.6	16397	4	US-08-956-171E-205
98	28.6	20.6	16397	4	US-08-956-171E-205
99	28.6	20.6	16397	4	US-08-956-171E-205
100	28.6	20.6	16397	4	US-08-956-171E-205

Sequence 205, Appl
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Sequence 84, Appl
Sequence 57, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 391, Appl
Sequence 391, Appl
Sequence 188, Appl
Sequence 188, Appl
Sequence 2641, Ap
Sequence 1734, Ap
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Sequence 187, Ap
Sequence 3761, Ap
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Sequence 69, Appl
Sequence 473, Ap
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Sequence 15, Appl
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Sequence 109, Ap
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Sequence 1264, Ap
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Sequence 2473, Ap
Sequence 1074, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 26700, A
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Sequence 11168, A
Sequence 398, Ap
Sequence 1901, Ap
Sequence 4365, Ap
Sequence 34365, A
Sequence 6, Appl
Sequence 6, Appl
Sequence 16, Appl
Sequence 15733, A
Sequence 24, Appl
Sequence 26, Appl
Sequence 1109, Ap
Sequence 3, Appl
Sequence 3527, Ap

ALIGNMENTS

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RESULT 1
US-09-439-313-293
; Sequence 293, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-293

Query Match      21.4%; Score 29.8; DB 3; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
|||
Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126

RESULT 2
US-09-352-616A-293
; Sequence 293, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-293

Query Match      21.4%; Score 29.8; DB 3; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
|||
Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126

RESULT 3
US-09-232-149A-293
; Sequence 293, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-293

Query Match      21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
|||
Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126

RESULT 4
US-09-159-812-293
; Sequence 293, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-293

Query Match      21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
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Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126
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QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
|||
Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126

RESULT 3
US-09-232-149A-293
; Sequence 293, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-293

Query Match      21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
|||
Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126

RESULT 4
US-09-159-812-293
; Sequence 293, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-293

Query Match      21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCAAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTTAGTCACTTCTGATTCGACAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
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Db 90 AATCAATCAATGGCTAGAGCACTGACTGTTAAACACA 126
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Db 90 AATCAATCAATGGCGCTAGAGCACTGACTGTTAAACACA 126
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RESULT 5
US-09-636-215-293
; Sequence 293, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-293

Query Match 21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGTTTAACTGTTTATCCCAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTTTGTGTAGTCACTTCTGATTCTGACAATC 89
|||||

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
|||||
Db 90 AATCAATCAATGGCGCTAGAGCACTGACTGTTAAACACA 126
|||||

RESULT 7
US-09-688-489-293
; Sequence 293, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-293

Query Match 21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGTTTAACTGTTTATCCCAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTTTGTGTAGTCACTTCTGATTCTGACAATC 89
|||||

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
|||||
Db 90 AATCAATCAATGGCGCTAGAGCACTGACTGTTAAACACA 126
|||||

RESULT 8
US-09-679-426-293
; Sequence 293, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-293

Query Match 21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGTTTAACTGTTTATCCCAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTTTGTGTAGTCACTTCTGATTCTGACAATC 89
|||||

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
|||||
Db 90 AATCAATCAATGGCGCTAGAGCACTGACTGTTAAACACA 126
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RESULT 6
US-09-685-166A-293
; Sequence 293, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-293

Query Match 21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCTGTTTAACTGTTTATCCCAAGCA 102
|||
Db 30 CTGTTCTCACTGAAAGTCTGGCTAATGCTTTGTGTAGTCACTTCTGATTCTGACAATC 89
|||||

QY 103 CCATAATCAACGCTAGACTGTTCTTTATTGTTAAACACA 139
|||||
Db 90 AATCAATCAATGGCGCTAGAGCACTGACTGTTAAACACA 126
|||||
```

```
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-293

Query Match      21.4%; Score 29.8; DB 4; Length 301;
Best Local Similarity 56.7%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTTTATTAACTGTTATCCCAAGCA 102
Db 30 CTGTTCTCACTGAAAGTGGCTAAGCTCTTGTTAGTCACTCTGATTCGCAATC 89

QY 103 CCATAATCAACGCTAGACTGTTCTTATTTGTTAAACACA 139
Db 90 AATCAATCAATGGCCTAGACGACTGCTGTTAAACACA 126

RESULT 9
US-09-107-532A-1865/c
; Sequence 1865, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1865:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1140
; SEQUENCE DESCRIPTION: SEQ ID NO: 1865:
US-09-107-532A-1865

Query Match      21.4%; Score 29.8; DB 4; Length 1140;
Best Local Similarity 66.2%; Pred. No. 0.76;
Matches 43; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 30 CCTGCCTCACCCTCTTTCTTCAGAAAGAGGGTGACTATTGTCGTTTATTAACTGTT 89
Db 431 CCTAGTTCACCCACTTCTTCTCCGACAGTGGCTAATAATTGACTGTTCCGTTAAATGTT 372

QY 90 TATCC 94
Db 371 TTTC 367

RESULT 10
US-09-673-395A-82/c
; Sequence 82, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 2143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-82

Query Match      21.4%; Score 29.8; DB 4; Length 2143;
Best Local Similarity 56.7%; Pred. No. 1;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTCAGAAAGGGTGACTATTGTCGTTTATTAACTGTTTATCCCAAGCA 102
Db 1254 CTGTTCTCACTGAAAGTCTGGCTAATGCTCTTGTGTAGTCACTCTGATTCGCAATC 1195

QY 103 CCATAATCAACGCTAGACTGTTCTTATTTGTTAAACACA 139
Db 1194 AATCAATCAATGGCCTAGACGACTGACTGTTAAACACA 1158

RESULT 11
US-09-489-847-86
; Sequence 86, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI
```

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; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-489-847-86

Query Match      21.4%; Score 29.8; DB 4; Length 3174;
Best Local Similarity 56.7%; Pred. No. 1.2;
Matches 55; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 43 CTTTCTTTCAGAAAGGGTGACTATTTGTCTGTTTATTAAGTCTTATCCCAAGCA 102
    |||||
Db 1767 CTGTTCTCACTGAAAGTGGCTAATGCTTGTGTAGTCACTTCTGATTCTGACAATC 1826

QY 103 CCATATCAAGCTAGACTGTTCTTTATTTGTTAACA 139
    |||||
Db 1827 AATCAATCAATGGCTAGAGCACTGCTGTTAACA 1863

RESULT 12
US-08-961-527-52/c
; Sequence 52, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-714-918-71

Query Match      20.9%; Score 29; DB 3; Length 3010;
Best Local Similarity 52.5%; Pred. No. 2.2;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 7 CTGGTCGACGAACCTTAATAATCCCTGCTCACCCTCTTTCTTCAGAAAGGGTGACT 66
    |||||
Db 1119 CTGCTTTAGTCGTTGAATAATTTCCGACAGCAACGTCAGGCTTTAAGATTAGCCGGANC 1178
```

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-52

Query Match      21.0%; Score 29.2; DB 4; Length 16593;
Best Local Similarity 81.0%; Pred. No. 3.9;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 39 CCCTCTTTTCTTCAGAAAGGGTGACTATTTGTCTGTTT 80
    |||||
Db 12443 CCCACCTTCTTCAGAAATGCTGCTGACTATCTGCTGGCTTA 12402

RESULT 13
US-08-714-918-71
; Sequence 71, Application US/08714918
; Patent No. 6037123
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ving
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmid, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,918
; FILING DATE: September 13, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 222/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-714-918-71

Query Match      20.9%; Score 29; DB 3; Length 3010;
Best Local Similarity 52.5%; Pred. No. 2.2;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 7 CTGGTCGACGAACCTTAATAATCCCTGCTCACCCTCTTTCTTCAGAAAGGGTGACT 66
    |||||
Db 1119 CTGCTTTAGTCGTTGAATAATTTCCGACAGCAACGTCAGGCTTTAAGATTAGCCGGANC 1178
```

QY 67 ATTGTCTGCTTTATTAACTGTTTATCCCAAGCACCATTAATCAACGCTAGACTGTT 124
Db 1179 CTTTACCCTTTTATAGCAACATTGCTCTACAGGACATCCCATATTTAAGTCTATGCGCTTT 1236

RESULT 14

US-09-265-315-71
; Sequence 71, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/247

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3010 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-265-315-71

Query Match 20.9%; Score 29; DB 3; Length 3010;

Best Local Similarity 52.5%; Pred. No. 2.2;

Mismatches 0; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 7 CTGGTCGACGAACCTTAATAATGCTGCTCACCTCTCTTTCTTCAGAAAGAGGTGACT 66

Db 1119 CTGCTTTAGTCGCTTGAATAATTTCCGCGACGACGTCAGGCTCTTAAGATTAAAGCCGGANC 1178

QY 67 ATTGTCTGCTTTATTAACTGTTTATCCCAAGCACCATTAATCAACGCTAGACTGTT 124

Db 1179 CTTTACCCTTTTATAGCAACATTGCTCTACAGGACATCCCATATTTAAGTCTATGCGCTTT 1236

RESULT 15

US-09-265-315-71

; Sequence 71, Application US/09265315

; Patent No. 6187541

; GENERAL INFORMATION:

; APPLICANT: Benton, Bret

; APPLICANT: Lee, Ving J.

; APPLICANT: Malouin, Francois

; APPLICANT: Martin, Patrick K.

; APPLICANT: Schmid, Molly B.

; APPLICANT: Sun, Dongxu

; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS

; TITLE OF INVENTION: TARGET GENES

; NUMBER OF SEQUENCES: 111

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/265,315

; FILING DATE: March 9, 1999

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/714,918

; FILING DATE: September 13, 1996

; APPLICATION NUMBER: 60/009,102

; FILING DATE: December 22, 1995

; APPLICATION NUMBER: 60/003,798

; FILING DATE: September 15, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 240/247

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3010 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-265-315-71

Query Match 20.9%; Score 29; DB 3; Length 3010;

Best Local Similarity 52.5%; Pred. No. 2.2;

Mismatches 0; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 7 CTGGTCGACGAACCTTAATAATGCTGCTCACCTCTCTTTCTTCAGAAAGAGGTGACT 66

Db 1119 CTGCTTTAGTCGCTTGAATAATTTCCGCGACGACGTCAGGCTCTTAAGATTAAAGCCGGANC 1178

QY 67 ATTGTCTGCTTTATTAACTGTTTATCCCAAGCACCATTAATCAACGCTAGACTGTT 124

Db 1179 CTTTACCCTTTTATAGCAACATTGCTCTACAGGACATCCCATATTTAAGTCTATGCGCTTT 1236

RESULT 16

US-09-266-417-71

Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/527,745

FILING DATE: 17-Mar-2000

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 222/005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 3010 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-09-527-745-71

Query Match

Best Local Similarity

Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Score 29; DB 4; Length 3010;

Pred. No. 2.2;

Patent No. 5798224

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/268,161A

FILING DATE: June 27, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Young J. Suh

REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/32149

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

US-08-453-695A-113/c

Sequence 113, Application US/08453695A

Patent No. 5708143

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

ZIP: 60606

COMPUTER READABLE FORM:

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,695A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32658
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 2347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-453-695A-113

Query Match

Best Local Similarity

Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Score 28.8; DB 1; Length 2347;

Pred. No. 2.3;

Patent No. 5798224

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/268,161A

FILING DATE: June 27, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Young J. Suh

REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/32149

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

US-08-453-695A-113/c

Sequence 113, Application US/08268161A

Patent No. 5798224

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/268,161A

FILING DATE: June 27, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Young J. Suh

REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/32149

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

US-08-453-695A-113/c

Sequence 113, Application US/08268161A

Patent No. 5798224

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: Protocadherin Materials and Methods

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &

STREET: 233 South Wacker, 6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2347 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-268-161A-113

Query Match 20.7%; Score 28.8; DB 1; Length 2347;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 56 AGAGGGTGACTATTGCTGGTTTATTAACTGTTTATCCCAAGCACCATAATCAACGC 115
DB 366 AGATGGAGACTTTTCTCGGTCCAAATATTTCATGTCACCAATCTATAATAATTATCTA 307

QY 116 TAGACTGTTCTTATTGTTAA 135
DB 306 TTGACTTTTCTAATTTAAAA 287

RESULT 21
US-08-453-702A-113/c
; Sequence 113, Application US/08453702A
; Patent No. 5891706
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 18 JUN 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/263,161
; APPLICATION NUMBER:
; FILING DATE: 27 JUN 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Greta E. No. 6262237and
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/34703
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2347 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-453-702A-113

Query Match 20.7%; Score 28.8; DB 2; Length 2347;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 56 AGAGGGTGACTATTGCTGGTTTATTAACTGTTTATCCCAAGCACCATAATCAACGC 115
DB 366 AGATGGAGACTTTTCTCGGTCCAAATATTTCATGTCACCAATCTATAATAATTATCTA 307

QY 116 TAGACTGTTCTTATTGTTAA 135
DB 306 TTGACTTTTCTAATTTAAAA 287

RESULT 22
US-09-099-639-113/c
; Sequence 113, Application US/09099639
; Patent No. 6262237
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 233 South Wacker, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 18 JUN 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/263,161
; APPLICATION NUMBER:
; FILING DATE: 27 JUN 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Greta E. No. 6262237and
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/34703
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2347 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-099-639-113

Query Match 20.7%; Score 28.8; DB 3; Length 2347;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 56 AGAGGGTGACTATTGCTGGTTTATTAACTGTTTATCCCAAGCACCATAATCAACGC 115
DB 366 AGATGGAGACTTTTCTCGGTCCAAATATTTCATGTCACCAATCTATAATAATTATCTA 307

QY 116 TAGACTGTTCTTATTGTTAA 135
DB 306 TTGACTTTTCTAATTTAAAA 287

RESULT 23
PCT-US95-08071-113/c
; Sequence 113, Application PC/TUS9508071
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: Protocadherin Materials and Methods
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08071
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 2347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-08071-113

Query Match 20.7%; Score 28.8; DB 5; Length 2347;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 56 AGAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGCACCATAATCAACGC 115
DB 366 AGATGAGACTTTTTCGGTCAAAATATTCATGTCACCATCTATTAATATCTA 307
QY 116 TAGACTGTTCTTATGTTAA 135
DB 306 TTGACTTTTCTAATTTAAAA 287

RESULT 24
US-09-212-971-11/c
Sequence 11, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2676
TYPE: DNA
ORGANISM: Mus musculus
US-09-212-971-11
Query Match 20.6%; Score 28.6; DB 3; Length 2676;
Best Local Similarity 64.2%; Pred. No. 2.9;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 42 TCTTTTCTTCAGAAAGAGGGTGACTATTGTCGTGTTTAACTGTTTATCCCAAGC 101
DB 2671 TTTTCTTTAAAAAAGAGGTATATGTCGTTTAACTTTTCTCACAATTC 2612
QY 102 ACCATAA 108
DB 2611 TTTATAA 2605

RESULT 25
US-08-800-929A-11/c
Sequence 11, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-11

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Query Match      20.6%; Score 28.6; DB 3; Length 2676;
Best Local Similarity 64.2%; Pred. No. 2.9;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 42 TCTTTTCTTCAGAAAGAGGTGACTATTTCCTGCTGTTTATTAACCTGTTATCCCAAAGC 101
    |||||
Db 2671 TTTTCTTTTAAAAAAGAGGTAATTATGTTGCTTTATTAACCTTTTCTCACAATTC 2612

QY 102 ACCATAA 108
    |||||
Db 2611 TTTATAA 2605

RESULT 26
US-09-617-053A-11/c
; Sequence 11, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-11

Query Match      20.6%; Score 28.6; DB 3; Length 2676;
Best Local Similarity 64.2%; Pred. No. 2.9;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 42 TCTTTTCTTCAGAAAGAGGTGACTATTTCCTGCTGTTTATTAACCTGTTATCCCAAAGC 101
    |||||
Db 2671 TTTTCTTTTAAAAAAGAGGTAATTATGTTGCTTTATTAACCTTTTCTCACAATTC 2612

QY 102 ACCATAA 108
    |||||
Db 2611 TTTATAA 2605

RESULT 27
US-08-956-171E-205/c
; Sequence 205, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; APPLICANT: Gil H. Choi
; APPLICANT: Patrick S. Dillon
; APPLICANT: Craig A. Rosen
; APPLICANT: Steven C. Barash
; APPLICANT: Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 16397 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-08-956-171E-205

Query Match      20.6%; Score 28.6; DB 4; Length 16397;
Best Local Similarity 53.9%; Pred. No. 6.3;
Matches 55; Conservative 1; Mismatches 46; Indels 0; Gaps 0;

QY 14 ACGAACTTAATAATGCGCTGCCTCACCCCTCTTTTCTTCAGAAAGAGGTGACTATTGTC 73
    |||||
Db 4185 ACTAACTTAATAATCAACGTTTAATGGNAATTTCAATACCGTGGTATCCGTACCG 4126

QY 74 TGGTTTATTAACTGTTTATCCCAAGACACCATATCAACGC 115
    |||||
Db 4125 TCGTGGTTTACCAGTTGCTGGTCAAAAAACGAAAAACMACGC 4084

RESULT 28
US-08-781-986A-205/c
; Sequence 205, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
```

RESULT 30
US-08-599-252-84/c
; Sequence 84, Application US/08599252
; Patent No. 5705343
; GENERAL INFORMATION:
; APPLICANT: DRAYNA, DENNIS T.
; APPLICANT: FEDER, JOHN N.

Search completed: December 22, 2004, 03:32:09
Job time : 75 secs

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OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 01:40:57 ; Search time 1743 Seconds
(without alignments)
2905.980 Million cell updates/sec

Title: us-10-070-882a-2
Perfect score: 139
Sequence: 1 gtagactcgtgacgaact.....ctgtttattgttaacaca 139

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc1:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	34.8	25.0	3932	3	AK082454 Mus muscu
2	34.4	24.7	414	6	BY642267 BY642267
3	33.6	24.2	204	1	AV231406 AV231406
4	33.6	24.2	274	2	BB775700 BB775700
5	33.6	24.2	318	2	BB094276 BB094276
6	33.6	24.2	335	2	BB222962 BB222962
7	33.6	24.2	448	5	BY439440 BY439440
C 8	33.6	24.2	570	8	AZ435636 1M0222H14
9	33.6	24.2	590	2	BE131381 L48-1355T
10	33.6	24.2	605	4	BM658097 MCR059H01
11	33.6	24.2	625	6	CAB835622 MCS039B06
12	33.6	24.2	633	6	CAB834105 MCS028H02
13	33.6	24.2	674	4	BM301497 MCR046F12
14	33.6	24.2	699	4	BM301422 MCR045F12
15	33.6	24.2	746	9	CR303205 Medicago
16	33.6	24.2	863	2	BE035174 M022809 M
17	33.6	24.2	866	9	CR308064 Medicago
18	33.6	24.2	889	9	CG952370 MBEAT30TR
19	33.6	24.2	1192	2	BE037111 MF15B07 M
C 20	33.4	24.0	521	8	AQ830244 HS 4825_B
21	33.4	24.0	728	9	AG308530 Mus muscu
C 22	33.4	24.0	957	6	CA791309 AGENCOURT
23	33.2	23.9	205	2	BB004186 BB004186
24	33	23.7	467	8	BZ915818 CH240_59A

```

c 98 30.6 22.0 453 1 AJ574756 AJ574756
c 99 30.6 22.0 465 2 BE687044 BE687044 uv92f06.Y
c 100 30.6 22.0 564 4 BG985735 BG985735 2734 NICH

ALIGNMENTS

RESULT 1
AK082454/c
LOCUS      3932 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
             enriched library, clone:C230052F14 product:unclassified, full
             insert sequence.
ACCESSION  AK082454
VERSION     AK082454.1 GI:26100683
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS
1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
REFERENCE   5
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
MEDLINE     12033323
PUBMED      12033323
REFERENCE   6
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingehashi, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE       Direct Submission

JOURNAL
SUBMITTED (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL: http://genome.gsc.riken.jp/
             URL: http://fantom.gsc.riken.jp/.
FEATURES
             Location/Qualifiers
             1..3932
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="PANTOM:DB:C230052F14"
                /db_xref="taxon:10090"
                /clone="C230052F14"
                /tissue_type="cerebellum"
                /clone_lib="RIKEN full-length enriched mouse cDNA library"
                /dev_stage="0 day neonate"
             misc_feature
             1..3932
                /note="unclassified"
ORIGIN
Query Match      25.0%; Score 34.8; DB 3; Length 3932;
Best Local Similarity 54.8%; Pred. No. 13;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY      14  ACGAATTAAATAATGCGCTCACCCCTCTTTCTTCAGAAAGGGGACTATTGTC 73
DB      2194  ACTATCTCATTTAAAGCTCTCTCATCTGTGTATATAATGTTGTGTAGGATTTTG 2135
QY      74  TGGTTTATTAACTGTTTATCCCAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
DB      2134  TGGTATATGACTGATTTTCTCAGATACATGTAATAATGTTGATGATCAAAAGTGT 2075
QY      134  AACACA 139
DB      2074  CAAGCA 2069

RESULT 2
BY642267
LOCUS      414 bp      mRNA      linear      EST 15-DEC-2002
DEFINITION cDNA clone K430350A22 3', mRNA sequence.
ACCESSION  BY642267
VERSION     BY642267.1 GI:26977449
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 414)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Ohsato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kenapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
Chochra, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

```


RESULT 7
 BY439440
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

BY439440 448 bp mRNA linear EST 13-DEC-2002
 BY439440 RIKEN full-length enriched, pooled tissues, 16 days
 embryo, etc. Mus musculus cDNA clone 1920162D12 3', mRNA sequence.
 BY439440.1 GI:26723810
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 448)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Choithia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawai, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reid, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wyszewski, B. A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome

FEATURES
 source

1. 448
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone_lib="RIKEN full-length enriched, pooled tissues, 16
 days embryo, etc."
 /notes="pooled tissues: (dev_stage=16 days
 embryo, tissue_type=heart, sex=mix), (dev_stage=16 days
 embryo, tissue_type=kidney, sex=mix), (dev_stage=17 days
 embryo, tissue_type=heart, sex=mix), (dev_stage=17 days
 embryo, tissue_type=stomach, sex=mix), (dev_stage=17 days
 embryo, tissue_type=kidney, sex=mix), (dev_stage=17 days
 pregnant, adult, tissue_type=amnio, sex=female),
 (dev_stage=13 days embryo, tissue_type=liver, sex=mix)"

ORIGIN

Query Match 24.2%; Score 33.6; DB 5; Length 448;
 Best Local Similarity 61.4%; Pred. No. 20;
 Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 47 TCTTGAAGAAGGGGAGCTATTGTCGTGTTTATTAACCTGTTATCCCAAGCACCAT 106
 |||||
 Db 262 TCTTCTGAGCTGTCGGTCCACTGTTTCAGATCTCTTCACTGTTTTTCTTCAGAGCAGCCC 321
 |||||
 QY 107 AATCAAGCTAGACTGTTCTTATTGTTA 134
 |||||
 Db 322 ACACATTGCTTGACAGTCTTGTGTGCA 349

RESULT 8
 AZ435636/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AZ435636 570 bp DNA linear GSS 03-OCT-2000
 1M0222H14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0222H14 R, genomic survey sequence.
 AZ435636
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 570)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Plasmid whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0222 row: H column: 14
 Seq primer: CACACAGGAAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 570.
 Location/Qualifiers
 1. 570
 /organism="Mus musculus"

RESULT 13
BM301497
LOCUS
DEFINITION

hours NaCl treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCR045F12 5, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM301497

BM301497.1 GI:18023872

EST.

Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Alzooaceae; Mesembryanthemum.

1 (bases 1 to 674)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

An expressed sequence tag database for the common ice plant,

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 046 row: F column: 12

Seq primer: T3 20mer

High quality sequence stop: 674.

FEATURES

source

1. .674

/organism="Mesembryanthemum crystallinum"

/mol_type="mRNA"

/db_xref="taxon:3544"

/clone="MCR045F12"

/tissue_type="leaf"

/dev_stage="six-week-old"

/clone_lib="Ice plant Lambda Uni-Zap XR expression

library, 48 hours NaCl treatment prescreened for removal

of highly abundant transcripts"

/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

ORIGIN

Query Match 24.2%; Score 33.6; DB 4; Length 674;
Best Local Similarity 61.4%; Pred. No. 22;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 44 TTTTCTCAGAAAGAGGGTGACTATTGTCTGTTTATTAACTGTTTATCCCAAGAC 103

DB 156 TTTTCATCACAAGAGCGTGACTTTGGGTTGAAATTCTTATCCCTTAATCAACAATCAC 215

QY 104 CATAATCAACGCTAGACTGTTCTTATTG 131

DB 216 CTGAAAAACAGTGGAGTTGTTTGTG 243

RESULT 14

BM301422

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Alzooaceae; Mesembryanthemum.

1 (bases 1 to 699)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM301422 699 bp mRNA linear EST 22-JAN-2002
MCR045F12 25886 Ice plant Lambda Uni-Zap XR expression library, 48
hours NaCl treatment prescreened for removal of highly abundant
transcripts Mesembryanthemum crystallinum cDNA clone MCR045F12 5,
mRNA sequence.

BM301422

BM301422.1 GI:18023797

EST.

Mesembryanthemum crystallinum (common iceplant)

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Alzooaceae; Mesembryanthemum.

1 (bases 1 to 699)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AUTHORS

TITLE

JOURNAL

COMMENT

Cushman, J.C.

An expressed sequence tag database for the common ice plant,

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 045 row: F column: 12

Seq primer: T3 20mer

High quality sequence stop: 699.

FEATURES

source

1. .699

/organism="Mesembryanthemum crystallinum"

/mol_type="mRNA"

/db_xref="taxon:3544"

/clone="MCR045F12"

/tissue_type="leaf"

/dev_stage="six-week-old"

/clone_lib="Ice plant Lambda Uni-Zap XR expression

library, 48 hours NaCl treatment prescreened for removal

of highly abundant transcripts"

/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

ORIGIN

Query Match 24.2%; Score 33.6; DB 4; Length 699;

Best Local Similarity 61.4%; Pred. No. 22;

Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 44 TTTTCTCAGAAAGAGGGTGACTATTGTCTGTTTATTAACTGTTTATCCCAAGAC 103

DB 156 TTTTCATCACAAGAGCGTGACTTTGGGTTGAAATTCTTATCCCTTAATCAACAATCAC 215

QY 104 CATAATCAACGCTAGACTGTTCTTATTG 131

DB 216 CTGAAAAACAGTGGAGTTGTTTGTG 243

RESULT 15

CR303205

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CR303205 746 bp DNA linear GSS 28-FEB-2004
Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.

CR303205

CR303205.1 GI:44708225

GSS.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 746)

Genoscope.

Direct Submission

Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Location/Qualifiers

1. .746

/organism="Medicago truncatula"

/mol_type="genomic DNA"

/cultivar="Jemalong A17"

/db_xref="taxon:3880"

/clone_lib="MTE1"

/note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI

```

; Debellie F. and Chalhoub B.-Genoscope sequence ID :
mte1-21P8FM1"

ORIGIN
Query Match          24.2%; Score 33.6; DB 9; Length 746;
Best Local Similarity 61.4%; Pred. No. 23;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 50 TCAGAAAGAGGGTGACTATTGCTGCTGTTTATTAACTGTTTATCCCAAGCACCATAAT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 517 TGATTAAAGAGTGTAGTATTAGTCAATTACATACATATATCCCAAGAGGACCACAT 576

QY 110 CAACGCTAGACTGTTCTTTATTGTTAAACA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 CAATGATATACTATATCCAAAATGAACA 604

RESULT 16
BE035174
LOCUS
DEFINITION
MO22B09 MO Mesembryanthemum crystallinum cDNA 5' similar to
drought-induced protein d119, mRNA sequence.
ACCESSION
BE035174
VERSION
BE035174.1 GI:8330298
KEYWORDS
EST.
SOURCE
Mesembryanthemum crystallinum (common iceplant)
ORGANISM
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE
1 (bases 1 to 863)
AUTHORS
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferrea, H., Kawasaki, S., McColough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
TITLE
Functional Genomics of Plant Stress Tolerance
JOURNAL
Unpublished (2000)
COMMENT
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
FEATURES
source
Location/Qualifiers
1..863
/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="5 weeks"
/clone_lib="MO"
/notes="no stress"

ORIGIN
Query Match          24.2%; Score 33.6; DB 2; Length 863;
Best Local Similarity 61.4%; Pred. No. 23;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 44 TTTTCTTCAGAAAGAGGGTGACTATTGCTGCTGTTTATTAACTGTTTATCCCAAGCAC 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 168 TTTTCATCAAAAGCAGGTGACTTTGCGTTGAAATCTTATCCCTAATCAACAATAC 227

QY 104 CATATCAACGCTAGACTGTTCTATTG 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 CTGAAAAAACAAGTGGGAGTTTGTGTTTG 255

RESULT 17
CR308064
LOCUS
DEFINITION
CR308064 Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.
ACCESSION
CR308064

```

```

CR308064.1 GI:44854208
GSS.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 866)
Genoscope.
Direct Submission
Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
FEATURES
source
Location/Qualifiers
1..866
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="WTE1"
/notes="Vector: pindigobac ; site 1: EcoRI ; Site 2: EcoRI
; Debellie F. and Chalhoub B.-Genoscope sequence ID :
mte1-29K6FM1"

ORIGIN
Query Match          24.2%; Score 33.6; DB 9; Length 866;
Best Local Similarity 61.4%; Pred. No. 23;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 50 TCAGAAAGAGGGTGACTATTGCTGCTGTTTATTAACTGTTTATCCCAAGCACCATAAT 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 TGATTAAAGAGTGTAGTATTAGTCAATTACATACATATATCCCAAGAGGACCACAT 575

QY 110 CAACGCTAGACTGTTCTTTATTGTTAAACA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 CAATGATATACTATATCCAAAATGAACA 603

RESULT 18
CG952370
LOCUS
DEFINITION
MBEAT30TR mth2 Medicago truncatula genomic clone 15F12, genomic
survey sequence.
ACCESSION
CG952370
VERSION
CG952370.1 GI:39864834
KEYWORDS
GSS.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 889)
TOWN, C.D., Shetty, J., Koo, H. and Feildblyum, T.F.
Sequencing of BAC ends from Medicago truncatula
Unpublished (2003)
Other GSSs: MBEAT30TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: CAGGAACAGCTATGACC
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..889
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="15F12"

```

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/clone_lib="mth2"
/notes="vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII; Cook, D.R. and Kim, D.J., unpublished"
ORIGIN
Query Match      24.2%; Score 33.6; DB 9; Length 889;
Best Local Similarity 63.8%; Pred. No. 23;
Matches 51; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 44 TTTTCTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCCAAGAC 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 TATTGATGATTAGAGAGTGATGATTAGTCAATACATACATATATCCCAAGAG 415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 104 CATATCAACGCTAGACTGT 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 CATCATCAATGATATACTAT 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 19
BE037111
LOCUS
DEFINITION
  BE037111 1192 bp mRNA linear EST 07-JUN-2000
  MP15907 MP Mesembryanthemum crystallinum cDNA 5' similar to
  drought-induced protein di19, mRNA sequence.
ACCESSION
  BE037111
VERSION
  BE037111.1 GI:8332127
SOURCE
  Mesembryanthemum crystallinum (common iceplant)
ORGANISM
  Mesembryanthemum crystallinum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE
  1 (bases 1 to 1192)
  Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
  Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
  Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.
  Functional Genomics of Plant Stress Tolerance
  Unpublished (2000)
  Contact: Michalowski, C.B.
  University of Arizona
  Bio Sciences West room 513, Tucson, AZ 85721, USA
  Tel: 520-621-7982
  Fax: 520-621-1697
  Email: cbm@u.arizona.edu
  Insert Length: 1 Std Error: 0.00.
  Location/Qualifiers
    1..1192
    /organism="Mesembryanthemum crystallinum"
    /mol_type="mRNA"
    /db_xref="taxon:3544"
    /tissue_type="apical meristem and leaf primordia"
    /dev_stage="6 weeks"
    /clone_lib="Mp"
    /note="3 d 500mM NaCl"

ORIGIN
Query Match      24.2%; Score 33.6; DB 2; Length 1192;
Best Local Similarity 61.4%; Pred. No. 24;
Matches 54; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 44 TTTTCTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTTATCCCCAAGAC 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 TTTTCATCAGAAAGAGGGTGACTTTGGTTGAAATCTTATCCCTAATCAACAATCAC 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 104 CATATCAACGCTAGACTGTTCTATTG 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 232 CTGAAAAACAGTGGAGTTGTTTGTG 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 20
AQ830244/c
LOCUS
DEFINITION
  AQ830244 521 bp DNA linear GSS 27-AUG-1999
  HS_4825_B2_G12_SP6E CIT Approved Human Genomic Sperm Library D Homo
  sapiens genomic clone Plate=4825 Col=24 Row=N, genomic survey

```

```

sequence.
AQ830244
VERSION
  AQ830244.1 GI:5796306
SOURCE
  GSS.
ORGANISM
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 521)
  Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
  Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
  Hood, L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  PUBMED
  1049764
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones may be purchased from Research Genetics (info@resgen.com).
  BAC end Web Server: http://www.htsc.washington.edu
  Plate: 4825 row: N column: 24
  Seq primer: T7
  Class: BAC ends
  High quality sequence stop: 521.
  Location/Qualifiers
    1..521
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /clone="Plate=4825 Col=24 Row=N"
    /sex="male"
    /clone_lib="CIT Approved Human Genomic Sperm Library D"
    /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
    E-Coli DH10B"

ORIGIN
Query Match      24.0%; Score 33.4; DB 8; Length 521;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 67; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2 TGACTCTGTCGACGAACTTAATAATGCTGCTCACCTCTTTCTTCAGAAAGGG 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 407 TGACTCTGGGCAAGTCACATAAAGCTGCTCAGTCTCAATTTCTTTAGAAAAATAGG 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 62 TGACTATTGTCTGGTTTATTAACTGTTATCCCAAGCACCATAATCAACGCTAGACT 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 ATGCTAATAATAAAAGCAGCACTGCTCAAGGATTAGTACTATTAATGCAAAATG 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 122 GTT 124
    ||
Db 287 CTT 285
    ||

RESULT 21
AG308530
LOCUS
DEFINITION
  AG308530 728 bp DNA linear GSS 02-JUN-2004
  Mus musculus molossinus DNA, clone:MSG01-090D23.TJ, genomic survey
  sequence.
ACCESSION
  AG308530
VERSION
  AG308530.1 GI:47881484
SOURCE
  GSS.
ORGANISM
  Mus musculus molossinus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1
  Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

```


TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 728)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan
(E-mail: hattori@gscc.riken.jp, URL: http://hgc.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@gscc.riken.jp).
Tsukuba Institute of Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@gscc.riken.jp
PRIMERS
Sequencing : TV
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES
source
Location/Qualifiers
1..728
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-090D23.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 24.0%; Score 33.4; DB 9; Length 728;
Best Local Similarity 58.6%; Pred. No. 25;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 39 CCTCTTTTCTTCAGAAAGGGTGACTATTGTCGTGTTTAACTGTTATCCCCAA 98
|||||
Db 216 CCTCTTTTCTTACCTAGTACATACCTTTTATATACAGTGATTTGTCGTGTTCTAT 275
|||||

Qy 99 AGCACATATATACAGCTAGCTGTTCTTTATTTGTTAA 137
|||||
Dy 276 AGCAAAATATTACTCAAGCCTTACTTCTAATTATCA 314
|||||

RESULT 22
CA791309/c
LOCUS
DEFINITION
AGENCOURT 10304652 NICHG_XGC Emb1 xenopus laevis cDNA clone
CA791309
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 957)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1401 row: j column: 20
High quality sequence stop: 360.

FEATURES
source
Location/Qualifiers
1..957
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5161843"
/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHG_XGC Emb1"
/notes="Vector: pCMV-SF0R6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match 24.0%; Score 33.4; DB 6; Length 957;
Best Local Similarity 72.9%; Pred. No. 26;
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 21 TAAATAATCCTGCTCACCCTCTTTCTTCAGAAAGGGTGACTATTGTCGTGTTT 79
|||||
Dy 917 TAAATTTTCGGCGCCAGCGCTTTTCTTTTAAAGAGGGGGGACAAATTTGCGGGTTT 859
|||||

RESULT 23
BB004186
LOCUS
DEFINITION
BB004186 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732458014 3', mRNA sequence.
BB004186.1 GI:8093634
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 205)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A.,
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsukuba, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagasaki, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermolabile and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES

```

source
1. .205
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4732458014"
/sex="mixed"
/tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 10 day neonate
skin"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGATCCAGAGCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5', GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"
```

ORIGIN

```

Query Match      23.9%; Score 33.2; DB 2; Length 205;
Best Local Similarity 57.8%; Pred. No. 23;
Matches 59; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 35 CTCACCTCTTTCTTCAGAAAGAGGTCATTTGTCGTTTATTAACTGTTTATCC 94
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 13 CTCACCTCTCTTGTCTGAGCAGTCTCCCACTTTTCAGATCTTTTCACTGTTTCT 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 95 CCAAGCACCAATCAACGCTAGACTGTTCTTATTGTTAAC 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 73 TAGGACACCCACACATTCCTTGACATTCCTTGTGTCACC 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 24

```

BZ915818
LOCUS CH240_59A23.TV CHORI-240 Bos taurus genomic clone CH240_59A23,
DEFINITION genomic survey sequence.
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ACCESSION BZ915818
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```

VERSION BZ915818.1 GI:31641204
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KEYWORDS

```

SOURCE GSS.
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ORGANISM

```

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
```

REFERENCE

```

1 (bases 1 to 467)
Larkin, D.M., Everets-van der Wind, A., Rebeiz, M., Schweitzer, P.,
Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L.,
Womack, J.E., de Jong, P.J. and Lewin, H.A.
```

```

A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
Genome Sequence
```

JOURNAL

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Unpublished (2003)
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Contact: Harris Lewin
```

```

Department of Animal Sciences
```

University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)

Plate: 59 row: A column: 23

Seq primer: T7

Class: BAC ends.

FEATURES

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source
1. .467
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_59A23"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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ORIGIN

```

Query Match      23.7%; Score 33; DB 8; Length 467;
Best Local Similarity 58.8%; Pred. No. 31;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 18 ACTTAATAATGCTGCTCACCTCTTTTCTTCAGAAAGAGGTCATTTGTCGTGT 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 46 ACTTATTTGCTGGATTCCCTCCAGATGATTTCAACAAGAGCTGTAAGTTTTGTGAG 105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 78 TTATTAACGTGTTATCCCAAGACCACCAATCAACG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 106 TTATTATATGTAACTCAAAATAACAATGAGCAAG 142
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```

RESULT 25

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AV336201
```

LOCUS

```

DEFINITION
```

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ACCESSION
```

```

VERSION
```

```

KEYWORDS
```

```

SOURCE
```

```

ORGANISM
```

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REFERENCE
```

```

AUTHORS
```

```

AV336201 206 bp mRNA linear EST 11-NOV-1999
AV336201 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330583F07 3', mRNA sequence.
```

```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206)
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```

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsumura, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Tsunoda, H., Suzuki, H., Takahashi, F., Tateno, M., Tomimaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
```

```

RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
```

```

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
```

B2035953.1 GI:23614280
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

high quality sequence. Stc0p: 551.
Location/Qualifiers
1. .690
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="vector: pOTw13; whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

BB230680 252 bp mRNA linear EST 04-JUL-2000
BB230680 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630028L21 3', mRNA sequence.

Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T.,
Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
Tomonaga, N., Toyota, T., Tsunoda, Y., Watanishi, A.,
Watanabe, S., Yamamoto, T., Yamanaka, I., Yano, R., Yasunishi, A.,

TITLE Yokota,T., Yoshida,K., Yoshiaki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
JOURNAL RIKEN Mouse ESTs (Konno,H., et al.)
COMMENT Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resesc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kiteunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
1. .252
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="Ac30028L21"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
/notes="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGATCCAGAGCTCTTTTTCCTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGATTCTCGAGTTAATAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda Flc I."

[illegible]

DEFINITION BB118576 RIKEN full-length enriched, adult male urinary bladder Mus musculus cDNA clone 9530066116 3', mRNA sequence.
ACCESSION BB118576
VERSION BB118576.1 GI:8771144
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 270)
AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs (Konno, H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermolabile and thermolabile enzymes by thermal inactivation and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Kitzunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for

```

FEATURES
source
location/Qualifiers
1. .270
/organism="Mus musculus"
/mol_type="mRNA"
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/clone="9530066116"
/sex="male"
/tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCCAAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of

```

CONTACT: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-5222
Fax: 81-45-503-5216
Email: genome-res@gs.c.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

MEDLINE 93380589
 PUBMED 10449764
 COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3169 row: B column: 11
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 906.

FEATURES

source
 1. .906
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3169 Col=11 Row=B"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelobAC11; BAC clones in
 E-Coli DH10B"

ORIGIN

Query Match 23.3%; Score 32.4; DB 8; Length 906;
 Best Local Similarity 56.6%; Pred. No. 53;
 Matches 60; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 QY 34 CCTCACCCCTCTTTTTCAGAAAGAGGGTGACTATTGTCTGGTTTATTAACTGTTTATC 93
 Db 690 CCCCCCTCTCTTTTAAAAAAGAGGGTTTGATTTTTTTTTTTTTTTTTTTTCTC 749
 QY 94 CCAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAAACACA 139
 Db 750 TTTCCCCCCCCCAAAAAAAACCCCTCCTCGTTGTGGGAAAAA 795

Search completed: December 22, 2004, 03:30:59
 Job time : 1755 secs

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